

GenCore version 5.1.3
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Om protein - protein search, using sw model

Run on: February 11, 2003, 18:21:26 ; Search time: 82 seconds
(without alignments)
30.875 Million cells updates/sec

title: US-09-781-796B-7
perfect score: 96
Sequence: 1 KSDIQTYGALDGCASTQ 19

Scoring table: BL2USM62 Gapov 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002:*

1: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1980.DAT:*

2: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1981.DAT:*

3: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1983.DAT:*

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6: /SIDS2/gcdata/geneseq/geneseq-emb1/AA1986.DAT:*

7: /SIDS2/gcdata/geneseq/geneseq-emb1/AA1987.DAT:*

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22: /SIDS2/gcdata/geneseq/geneseq-emb1/AA2002.DAT:*

23: /SIDS2/gcdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB ID	Description
1	96	100.0	20	ATP diphosphohydroxy
2	82	85.4	16	ATP diphosphohydroxy
3	75	78.1	43	Soluble human CD39
4	75	78.1	454	Protein encoded by Human soluble CD39
5	75	78.1	454	Human soluble CD39
6	75	78.1	453	Protein encoded by Human soluble CD39
7	75	78.1	463	Protein encoded by Human soluble CD39
8	75	78.1	464	Protein encoded by Human soluble CD39
9	75	78.1	464	Protein encoded by Human soluble CD39
10	75	78.1	473	Protein encoded by Human soluble CD39

RESULT 1
ID AAM04339
AC AAM04339;
XX DT 29-DEC-1996 (first entry)
DE ATP diphosphohydrolase fragment from pig pancreas.
KW ATP diphosphohydrolase; ATPDase; bovine aorta; pig pancreas;
KW apyrase; CD39; lymphoid cell activation antigen; enzyme;
KW platelet aggregation; thrombogenicity; anti-haemostatic;
OS Sus scrofa.
PN W09632471-A2
PD 17-OCT-1996.
PF 10-APR-1996; 96WO-CA00223.
PR 10-APR-1995; 95US 0419204.
XX PA (UWSH) UNIV SHERBROOKE.
XX PI Beaudoin AR, Sevigny J;
XX DR WPI: 1996-47112/47.
XX PT Isolated ATP di-phosphohydrolase enzymes - have anti-haemostatic activity, useful for reducing platelet aggregation and thrombogenicity

XX
 PS Claim 3; Page 46; 60pp; English.
 XX
 CC The bovine aorta (AAW04335 to AAW04338 and AAW04340) and porcine
 CC pancreatic (AAW04339) ATPases have been partially sequenced.
 CC The sequences have been found to be highly homologous to a human
 CC lymphoid cell activation antigen designated CD39 (Malszinski et
 CC al. (1994); J. Immunol.: 3574-3583). The complete sequences of the
 CC ATPases types I and II have not been obtained yet. Assuming that
 CC the CD39 gene product is an ATPase type II, the use of CD39
 CC in the reduction of platelet aggregation and of thrombogenicity
 CC may be contemplated, as well as a process of making ATPases
 CC using the CD39 sequence (AAT38516).
 XX Sequence 20 AA;
 SQ Query Match 85.4%; Score 82; DB 17; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KSDTQETYGAIDLGGA 16
 Db 1 KSDTQETYGAIDLGGA 16
 RESULT 2
 AAW04340
 ID AAW04340 standard; Protein; 16 AA.
 XX AC AAW04340;
 XX AC AAB71918;
 XX DT 09-MAY-2001 (first entry)
 XX DE Soluble human CD39 polypeptide.
 XX KW Human; CD39; vasotropic; cerebroprotective; haemostatic; thrombolytic;
 XX KW stroke; thrombotic disorder; ischaemic disorder.
 OS Homo sapiens
 XX PN WO200111949-A1.
 XX PD 22-FEB-2001.
 XX PR 11-AUG-2000; 2000WO-US22060.
 XX PR 13-AUG-1999; 99US-0374586.
 XX PA (UFCO) UNIV COLUMBIA NEW YORK.
 PI Piskey DJ;
 XX DR WP1; 2001-202805/20.
 XX PT Treating stroke in a subject susceptible to intracranial hemorrhaging
 XX PT and an ischaemic disorder, involves administering a CD39 polypeptide
 XX PT which inhibits ADP-mediated platelet aggregation or leukocyte
 XX accumulation.
 PS Claim 3; Page 14; 118pp; English.
 XX
 The present sequence is the active fragment of human CD39. CD39 or its
 active fragment may be administered to treat or prevent stroke in a
 subject susceptible to intracranial haemorrhaging or an ischaemic
 disorder. The CD39 polypeptide inhibits ADP-mediated platelet aggregation
 or leukocyte accumulation and/or ADP by increasing ADP catabolism to the
 subject. CD39 or its active fragment is useful for treating or preventing
 stroke, thrombotic disorders and ischaemic disorders such as peripheral
 vascular disorder, pulmonary embolus, venous thrombosis, myocardial
 infarction, transient ischaemic attack, unstable angina, reversible
 ischaemic neurological deficit and sickle cell anaemia. It is also
 useful for treating or preventing a stroke disorder in a subject
 undergoing heart surgery, lung surgery, spinal surgery, brain surgery,
 vascular surgery, abdominal surgery, or organ transplantation surgery.
 XX Sequence 439 AA;
 SQ Query Match 78.1%; Score 75; DB 22; Length 439;
 Best Local Similarity 73.7%; Pred. No. 0.00011; Mismatches 14; Indels 1; Gaps 0;
 Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 KSDTQETYGAIDLGGA 19
 Db 165 ETNNOETFGALDGGASTQ 183
 RESULT 4
 AAY70890

Sequence 16 AA;

RESULT 4

PR 13-AUG-1999; 99US-0149010.
 XX
 PA (IMMUNEX CORP.
 XX
 PT Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
 XX
 DR WPI; 2000-339644/29.
 XX
 PT New soluble CD39 polypeptides having apyrase activity, useful for inhibiting angiogenesis and treating unstable angina, myocardial infarction, stroke, coronary artery disease or injury.
 XX
 PS Claim 6; Page 116-118; 12pp; English.
 XX
 CC The present sequence is the fusion protein construct, IgkappaSolCD39. This construct comprises of the leader peptide from human immunoglobulin Ig kappa, linked to the soluble CD39 (solCD39) protein region by few residues derived from human interleukin 2 (IL2). SolCD39 has apyrase activity and is constructed by removing the N- and C-terminal transmembrane domains. It retains the capacity to metabolise ATP and ADP at relevant concentrations and the ability to block and reverse ADP-induced platelet activation and recruitment, including platelet aggregation. Soluble CD39 polypeptides are useful for inhibiting angiogenesis. It is useful for the treatment of unstable angina, stroke, myocardial infarction, coronary artery disease or injury, embolism, atherosclerosis, peripheral vascular occlusion, preeclampsia, platelet-associated ischaemic disorders including lung, coronary and cerebral ischaemia, thrombotic disorders including coronary, Peripheral and cerebral artery thrombosis, intracardiac and venous thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or restenosis of blood vessels or stroke.
 XX
 SQ Sequence 463 AA:
 Query Match 78.1%; Score 75; DB 21; Length 463;
 Best Local Similarity 73.7%; Pred. No. 0.00012; Mismatches 14; Conservative 4; Indels 0; Gaps 0;
 Matches 1;
 CC
 QY 1 KSDTQETYGALDLGGASTQ 19
 ::::|11:|||||||||||
 DB 189 ETNNQETFGALDLGGASTQ 207
 XX
 RESULT 8
 AAY70899
 ID AAY70899 standard; Protein; 464 AA.
 XX
 AC AAY70899;
 XX
 DT 17-AUG-2000 (first entry)
 XX
 DE Protein encoded by Trim 1 construct.
 XX
 PT Soluble CD39: ADP-induced platelet activation; platelet aggregation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; lung ischaemia; thrombolytic; cerebral ischaemia; thrombotic disorder; coronary artery thrombosis; peripheral artery thrombosis; intracardiac thrombosis; venous thrombosis; peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT; PE; pulmonary embolism; transient ischaemic attack; thrombus formation; occlusion; reocclusion; stenosis; restenosis; antianginal; cardiotonic; cerebroprotective; antiarteriosclerotic; vasotropics; anticoagulant; coronary ischaemia; vascular occlusion; plb2trml variant; Homo sapiens. Synthetic.
 OS
 XX
 FH Key Cleavage-site Location/Qualifiers
 FT Protein 24..25
 FT Protein 26..464
 XX
 note= "Soluble portion of CD39"
 FT XX
 PN WO200023094-A2.
 XX
 PD 27-APR-2000.
 XX
 PR 13-OCT-1999; 99WO-US23641.
 XX
 PR 16-OCT-1998; 98US-0104585.
 PR 06 NOV-1998; 98US-0107466.
 PR 13-AUG-1999; 99US-0149010.
 XX
 PA (IMMUNEX CORP.
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Maliszewski CR, Gayle RB, Marcus AJ;
 XX
 DR WPI; 2000-339518/29.
 XX
 PT Inhibiting platelet activation and recruitment, useful for treating a mammal suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, comprises administering soluble CD39 polypeptides.
 PT
 PS Example 11; Page 111-112; 118pp; English.
 XX
 CC The present sequence is the protein encoded by triml construct. PIL2trml variant was constructed by removing the human IL2 residues from solCD39 fusion construct. Fusion of 12 amino acids from the N-terminus of mature human IL2 to the solCD39 coding region results in high levels of both expression and activity in the supernatants of transfected cells. SolCD39 is used in the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism, platelet-associated ischaemic disorder including lung ischaemia, coronary ischaemia and cerebral ischaemia, a thrombotic disorder including coronary artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, Peripheral artery thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or restenosis of blood vessels or stroke.
 XX
 SQ Sequence 464 AA:
 Query Match 78.1%; Score 75; DB 21; Length 464;
 Best Local Similarity 73.7%; Pred. No. 0.00012; Mismatches 14; Conservative 4; Indels 0; Gaps 0;
 Matches 1;
 CC
 QY 1 KSDTQETYGALDLGGASTQ 19
 ::::|11:|||||||||||
 DB 190 ETNNQETFGALDLGGASTQ 208
 XX
 RESULT 9
 AAY70922
 ID AAY70922 standard; Protein; 464 AA.
 XX
 AC AAY70922;
 XX
 DT 17-AUG-2000 (first entry)
 XX
 DE Human soluble CD39 fusion protein construct, pil2trml.
 XX
 PT Soluble CD39; solCD39; human; apyrase activity; platelet activation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE; thrombus formation; occlusion; stenosis; restenosis; angiogenesis; antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant; cardiotonic; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.

		OS	Homo sapiens.
XX		OS	Synthetic.
Key	Location/Qualifiers	KW	Soluble CD39; ADP-induced platelet activation; platelet aggregation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism;
Peptide	/Label= "leader peptide"	KW	platelet-associated ischaemic disorder; lung ischaemia; thrombolytic; cerebral ischaemia; thrombotic disorder; coronary artery thrombosis; cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis; peripheral artery thrombosis; coagulopathy; deep venous thrombosis; PE; pulmonary embolism; transient ischaemic attack; thrombus formation; occlusion; reocclusion; stenosis; restenosis; antiangiinal; cardiotonic; cerebroprotective; antiplatelet; vasodilator; vasoconstrictor; antiangiinal; coronary ischaemia; vascular occlusion; pil2trim4 variant.
FT	/note= "derived from human interleukin 2 (IL2)"	KW	Homo sapiens.
FT	/note= "Cleavage site of leader sequence"	KW	Synthetic.
FT	/note= "Human soluble CD39 protein"	KW	
Protein		PN	WO200023459-A1.
XX		PD	27-APR-2000.
XX		XX	
PF	13-OCT-1999; 99WO-US22955.	PR	16-OCT-1998; 98US-0104585.
XX		PR	06-NOV-1998; 98US-0107466.
PR	13-AUG-1999; 99US-0149010.	XX	
PA	(IMM) IMMUNEX CORP.	PN	
XX		PT	Maliszewski CR, Gayle RB, Price VL, Gimpel SD;
DR		XX	
XX		WPI; 2000-339644/29.	
PT	New soluble CD39 polypeptides having apyrase activity, useful for inhibiting angiogenesis and treating unstable angina, myocardial infarction, stroke, coronary artery disease or injury -	PR	16-OCT-1998; 98US-0104585.
PT	constructed comprises the leader peptide from human interleukin 2 (IL2) and soluble CD39 (solCD39) protein region, having apyrase activity. The two regions are joined by an intervening Ala residue. Soluble CD39 is constructed by removing the N- and C-terminal transmembrane domains. It retains the capacity to metabolise ATP and ADP at relevant concentrations and the ability to block and reverse ADP-induced platelet activation and recruitment, including platelet aggregation. Soluble CD39 polypeptides are useful for inhibiting angiogenesis. It is useful for the treatment of unstable angina, stroke, myocardial infarction, coronary artery disease or injury, embolism, atherosclerosis, peripheral vascular occlusion, preecclampsia, platelet-associated ischaemic disorders including lung, coronary and cerebral ischaemia, thrombotic disorders including coronary, peripheral and cerebral artery thrombosis, intracardiac and venous thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or restenosis of blood vessels or stroke.	PR	06-NOV-1998; 98US-0107466.
XX		PR	13-AUG-1999; 99US-0149010.
PS	Claim 6; Page 111-112; 12pp; English.	XX	
CC	The present sequence is the fusion protein construct, pil2triml. This construct comprises the leader peptide from human interleukin 2 (IL2) and soluble CD39 (solCD39) protein region, having apyrase activity. The two regions are joined by an intervening Ala residue. Soluble CD39 is constructed by removing the N- and C-terminal transmembrane domains. It retains the capacity to metabolise ATP and ADP at relevant concentrations and the ability to block and reverse ADP-induced platelet activation and recruitment, including platelet aggregation. Soluble CD39 polypeptides are useful for inhibiting angiogenesis. It is useful for the treatment of unstable angina, stroke, myocardial infarction, coronary artery disease or injury, embolism, atherosclerosis, peripheral vascular occlusion, preecclampsia, platelet-associated ischaemic disorders including lung, coronary and cerebral ischaemia, thrombotic disorders including coronary, peripheral and cerebral artery thrombosis, intracardiac and venous thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or restenosis of blood vessels or stroke.	XX	
CC	Sequence 464 AA;	XX	
CC	Query Match 78.1%; Score 75; DB 21; Length 464; Best Local Similarity 73.7%; Pred No. 0.00012; Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;	XX	
CC	QY 1 KSDTOETYGALDGASTQ 19	XX	
CC	DB 190 ETNQEQFGALDGASTQ 208	XX	
SQ	Sequence 464 AA;	XX	
RESULT 10		XX	
AYAY70901		Query Match 78.1%; Score 75; DB 21; Length 473; Best Local Similarity 73.7%; Pred. No. 0.00012; Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;	
ID AAY70901	standard; Protein; 473 AA.	XX	
AC AAY70901;		XX	
XX DT 17-AUG-2000 (first entry)		XX	
DE Protein encoded by Trim 4 construct.		XX	

CC ischaemia, a thrombotic disorder including coronary artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack.

CC Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or restenosis of blood vessels or stroke.

XX Sequence 474 AA;

Query Match 78.1%; Score 75; DB 21; Length 474;
Best Local Similarity 73.7%; Pred. No. 0.00012;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDTOETYGALDGGASTQ 19
::: |||:|||||:|||||:
Db 200 ETNNOETFGALDGGASTQ 218

RESULT 13

AAV70923 standard; Protein: 474 AA.

AC AAV70923;

XX DT 17-AUG-2000 (first entry)

DE Human soluble CD39 fusion protein construct, pIL2LTrim3.

XX Soluble CD39; solidCD39; human; apyrase activity; platelet activation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE; thrombus formation; occlusion; stenosis; restenosis; angiogenesis; antiangiinal; cerebroprotective; antiarteriosclerotic; anticoagulant; cardiant; vasoconstrictor; thrombolytic; inhibitor; interleukin 2; IL2.

OS Homo sapiens.
OS Synthetic.

XX

FH Key Location/Qualifiers
PT Peptide 1..24
FT /label= Leader_peptide
FT Cleavage-site 24..25
/note= "Derived from human interleukin 2 (hIL2)"
FT Protein 36..474
/note= "Cleavage site of leader sequence"
FT Protein 36..474
/note= "Human soluble CD39 protein"

PN WO200023459-AL.
XX
PD 27-APR-2000.
XX
PF 13-OCT-1999; 99WO-US22955.

XX PR 16-OCT-1998; 98US-0104585.
PR 06-NOV-1998; 98US-010466.
PR 13-AUG-1999; 99US-0149010.

PA (IMMUNEX) IMMUNEX CORP.
XX
PI Majszewski CR, Gayle RB, Price VL, Gimbel SD;
XX
DR WP1; 2000-339644/29.

XX
PT New soluble CD39 polypeptides having apyrase activity, useful for inhibiting angiogenesis and treating unstable angina, myocardial infarction, stroke, coronary artery disease or injury -
XX
PS Claim 6; Page 113-114; 122pp; English.

XX
CC The present sequence is the fusion protein construct, pIL2LTrim3. This

CC construct comprises of the leader peptide from human interleukin 2 (hIL2) and soluble CD39 (solCD39) protein region, having apyrase activity.

CC Soluble CD39 is constructed by removing the N- and C-terminal transmembrane domains. It retains the capacity to metabolise ATP and ADP at relevant concentrations and the ability to block and reverse ADP-induced platelet activation and recruitment, including platelet aggregation. Soluble CD39 polypeptides are useful for inhibiting angiogenesis. It is useful for the treatment of unstable angina, stroke, myocardial infarction, coronary artery disease or injury, embolism, atherosclerosis, peripheral vascular occlusion, preeclampsia, platelet-associated ischaemic disorders including lung, coronary and cerebral cerebral artery thrombosis, intracardiac and venous thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or restenosis of blood vessels or stroke.

XX Sequence 474 AA;

Query Match 78.1%; Score 75; DB 21; Length 474;
Best Local Similarity 73.7%; Pred. No. 0.00012;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDTOETYGALDGGASTQ 19
::: |||:|||||:|||||:
Db 200 ETNNOETFGALDGGASTQ 218

RESULT 14

AAV70888 standard; Protein: 476 AA.

AC AAV70888;

XX DT 17-AUG-2000 (first entry)

DE Protein encoded by CD39-L4-1 construct.

XX Soluble CD39; ADP-induced platelet activation; platelet aggregation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; lung ischaemia; thrombotic; cerebral ischaemia; thrombotic disorder; coronary artery thrombosis; cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis; peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DVT; PE; pulmonary embolism; transient ischaemic attack; thrombus formation; occlusion; reocclusion; stenosis; restenosis; antiangiinal; cardiant; cerebroprotective; antiarteriosclerotic; vasoconstrictor; thrombolytic; coronary ischaemia; vascular occlusion.

OS Homo sapiens.
OS Synthetic.

XX

FH Key Location/Qualifiers
PT Cleavage-site 20..21
FT Region 1..37
/note= "Derived from CD39-L4"
FT Region 38..476
/note= "Soluble portion of CD39"

XX PN WO200023094-A2.
XX
PD 27-APR-2000.
XX
PF 13-OCT-1999; 99WO-US23641.

XX PR 16-OCT-1998; 98US-0104585.
PR 06-NOV-1998; 98US-0107466.
PR 13-AUG-1999; 99US-0149010.

XX
PA (IMMUNEX) IMMUNEX CORP.
PA (CORR) CORNELL RES FOUND INC.

		FT	Region	49..476	/note= "soluble portion of CD39"
		FT			
XX		XX			
PT	Maliszewski CR, Gayle RB, Marcus AJ;				
XX		XX			
DR	WPI; 2000-339518/29.				
XX		XX			
PT	Inhibiting platelet activation and recruitment, useful for treating a mammal suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, comprises administering soluble CD39				
XX		XX			
PT	polypeptides -				
PS	Claim 6; Page 89-91; 118pp; English.				
XX		XX			
CC	The present sequence is a fusion construct of human soluble CD39 encoded by CD39-L4-1 construct. CD39-L4 is a secreted apyrase belonging to the CD39 family. The fusion construct is used for the expression and activity of soluble CD39 in CHO (chinese hamster ovary) cells. Soluble CD39 retains the capacity of wildtype CD39 to metabolise ATP and ADP at physiologically relevant concentrations as well as the ability to block reverse ADP-induced platelet activation and recruitment, including platelet aggregation. This is used in the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism, thrombus formation or reformation, occlusion, reocclusion, stenosis or restenosis of blood vessels or stroke.				
CC		XX			
CC	coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, stenosis or restenosis of blood vessels or stroke.				
CC		XX			
CC	artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous thrombosis, thrombosis, atherosclerosis, PeripheraL vascular occlusion, preeclampsia, embolism, platelet-associated ischaemic disorder including lung ischaemia, thrombotic disorder including coronary ischaemia and cerebral ischaemia, thrombosis, intracardiac thrombosis, artery thrombosis, cerebral artery thrombosis, thrombosis, thrombosis, atherosclerosis, PeripheraL vascular occlusion, preeclampsia, embolism, platelet-associated ischaemic disorder including lung ischaemia, thrombotic disorder including coronary ischaemia and cerebral ischaemia, thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, stenosis or restenosis of blood vessels or stroke.				
XX		XX			
SQ	Sequence 476 AA;				
Query Match	78.1%; Score 75; DB 21; Length 476;				
Best local Similarity	73.7%; Pred. No. 0.00012;				
Matches	14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;				
QY	1 KSDTQTYGALDGGSTQ 19				
Db	:::: : 220				
RESULT 15					
ID	AY70889				
ID	AY70889 standard; Protein: 476 AA.				
XX					
AC	AY70889;				
XX					
DT	17-AUG-2000 (first entry)				
XX					
DE	protein encoded by CD39-L4 construct.				
XX					
KW	Soluble CD39; ADP-induced platelet activation; platelet aggregation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; lung ischaemia; thrombolytic; coronary ischaemia; cerebr al ischaemia; coronary artery thrombosis; cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis; thrombosis, coagulopathy, deep venous thrombosis; DVT; PE; pulmonary embolism; transient ischaemic attack; thrombus formation; occlusion; reocclusion; stenosis; restenosis; antianginal; cardiotonic; cerebroprotective; antiarteriosclerotic; vasotropi c; anticoagulant; thrombotic disorder; vascular occlusion.				
KW					
OS	Homo sapiens.				
OS					
Synthetic.					
Key	Location/Qualifiers				
Misc-difference	39 /note= "Any amino acid preferably Cys or Ser"				
FT	20..21				
FT	Cleavage-site				
FT	1..48				
FT	Region /note= "Derived from CD39-L4"				

Query Match 78.1%; Score 75; DB 21; Length 476;

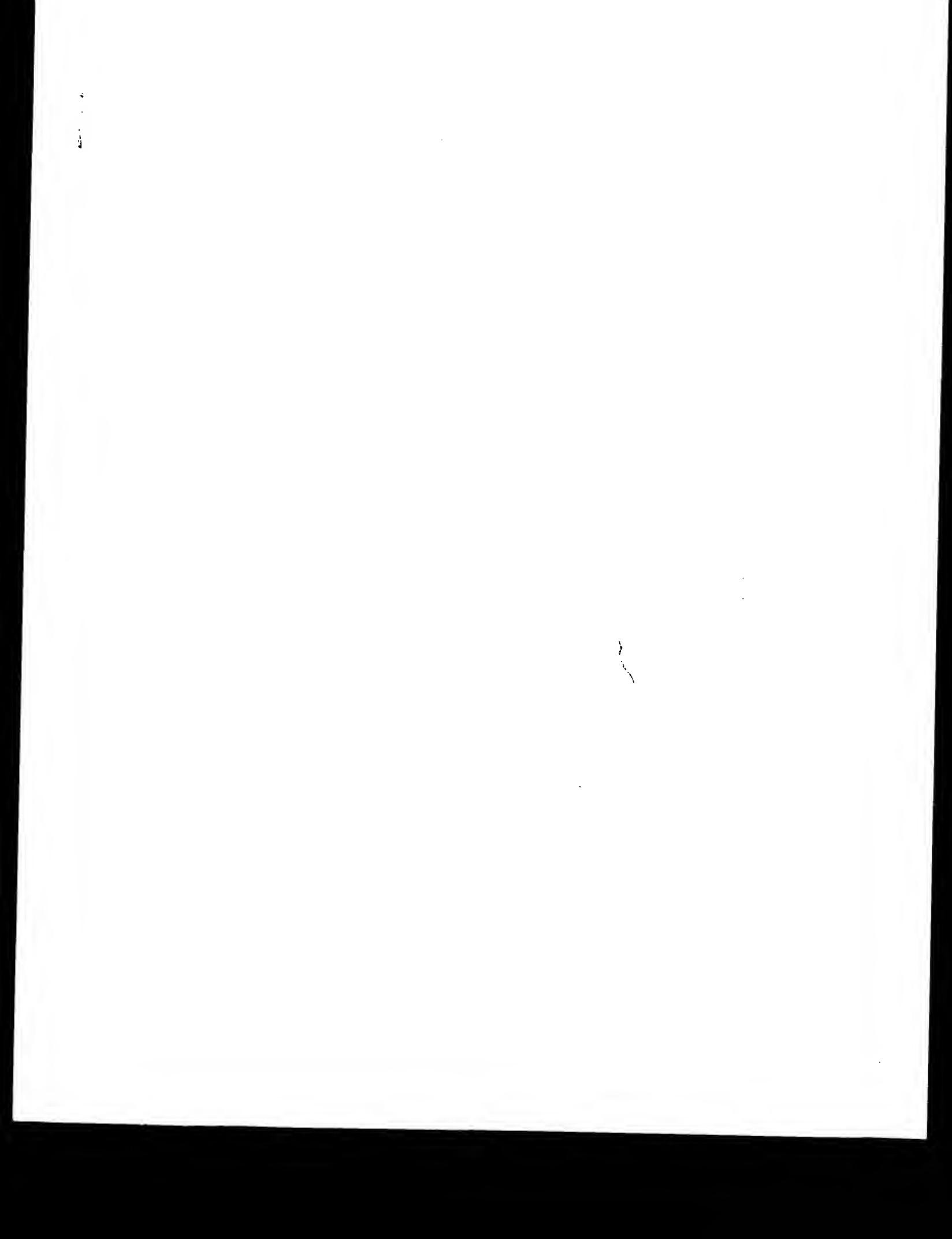
Best local Similarity 73.7%; Pred. No. 0.00012;

Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDTQTYGALDGGSTQ 19

Db :::: |||:||||||| 220

Search completed: February 11, 2003, 18:37:42
Job time : 83 secs



BioTech-Chem Library

Search Results

Feedback Form (Optional)



The search results generated for your recent request are attached. If you have any questions or comments (compliments or complaints) about the scope or the results of the search, please contact the BioTech searcher who conducted the search or contact:

Mary Hale, Supervisor, 3
CM-1 Room 1E01

Voluntary Results Feedback Form

➤ *I am an examiner in Workgroup:* (Example: 1610)

➤ *Relevant prior art found, search results used as follows:*

- 102 rejection
- 103 rejection
- Cited as being of interest.
- Helped examiner better understand the invention.
- Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

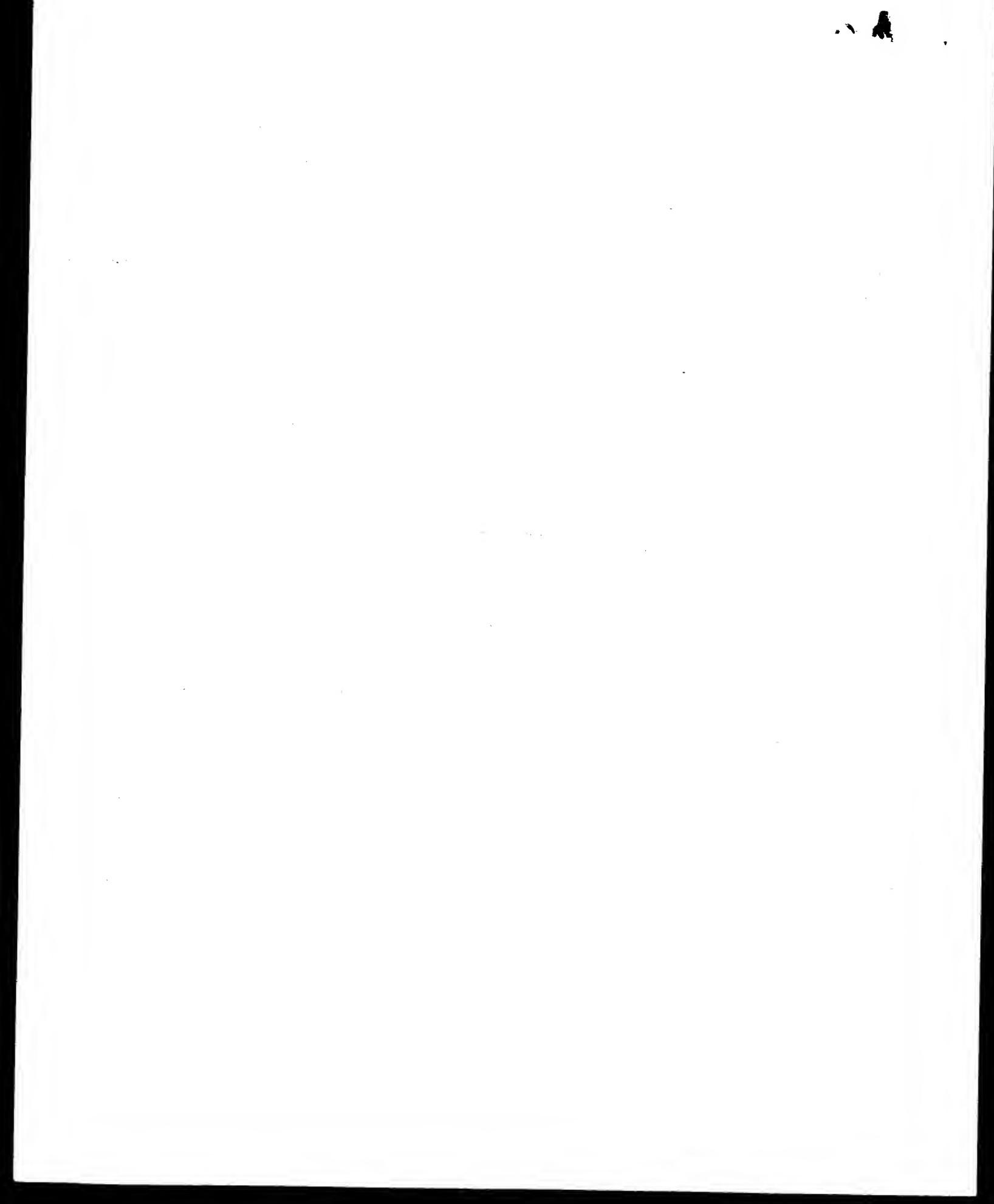
- Foreign Patent(s)
- Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ *Relevant prior art not found:*

- Results verified the lack of relevant prior art (helped determine patentability).
- Search results were not useful in determining patentability or understanding the in-

Other Comments:

Drop off completed forms at the Circulation Desk CM-1, or send to Mary Hale, CM1-1E01 or
mary.hale@uspto.gov




```

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: unknown
US-09-930-921-8
Query Match          85.4%; Score 82; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.5e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy      1 KSDTOETYGALDGGA 16
Db      1 KSDTOETYGALDGGA 16

RESULT 3
US-09-930-921-1
; Sequence 1, Application US/08930921B
; Patent No. 62B837
; GENERAL INFORMATION:
; APPLICANT: BEAUDOIN, Adrien R.
; APPLICANT: SEVIGNE, Jean
; TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
; TITLE OF INVENTION: TECHNOLOGY
; TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES - BRAUDOIN
; CURRENT APPLICATION NUMBER: US/08/930,921B
; CURRENT FILING DATE: 1998-01-02
; EARLIER APPLICATION NUMBER: PCT/CN96/00223
; EARLIER FILING DATE: 1995-04-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: unknown
US-09-930-921-1

Query Match          78.1%; Score 75; DB 4; Length 510;
Best Local Similarity 73.7%; Pred. No. 4.2e-05; Length 510;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Oy      1 KSDTOETYGALDGASTQ 19
Db      2 02 ETNNQETGALDGASTQ 220

RESULT 4
US-09-608-285A-25
; Sequence 25, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Muñoz, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 2111/35008
; CURRENT APPLICATION NUMBER: US/09/370,265
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: PCT/US99/16180
; EARLIER FILING DATE: 1999-07-16
; EARLIER APPLICATION NUMBER: 09/350,836
; EARLIER FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: 09/273,447
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: 09/244,444
; EARLIER FILING DATE: 1999-02-04
; EARLIER APPLICATION NUMBER: 09/122,449
; EARLIER FILING DATE: 1998-07-24
; EARLIER APPLICATION NUMBER: 09/118,205
; EARLIER FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-370-265-25

Query Match          66.7%; Score 64; DB 4; Length 405;
Best Local Similarity 86.7%; Pred. No. 0.0006; Mismatches 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy      5 QETYGALDGASTQ 19
Db      192 QETVGTLDSLGASTQ 206

RESULT 5
US-09-370-265-25
; Sequence 25, Application US/09370265
; Patent No. 644771
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Muñoz, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 2111/35008
; CURRENT APPLICATION NUMBER: US/09/370,265
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: PCT/US99/16180
; EARLIER FILING DATE: 1999-07-16
; EARLIER APPLICATION NUMBER: 09/350,836
; EARLIER FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: 09/273,447
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: 09/244,444
; EARLIER FILING DATE: 1999-02-04
; EARLIER APPLICATION NUMBER: 09/122,449
; EARLIER FILING DATE: 1998-07-24
; EARLIER APPLICATION NUMBER: 09/118,205
; EARLIER FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-370-265-25

Query Match          66.7%; Score 64; DB 4; Length 405;
Best Local Similarity 86.7%; Pred. No. 0.0006; Mismatches 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy      5 QETYGALDGASTQ 19
Db      192 QETVGTLDSLGASTQ 206

RESULT 6
US-09-608-285A-3
; Sequence 3, Application US/09608285A

```

Patent No. 6335013
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
FILE REFERENCE: 28110/36570
CURRENT APPLICATION NUMBER: US/09/608, 285A
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/583, 231
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 09/557, 800
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481, 238
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/370, 265
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350, 836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273, 447
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/244, 444
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/122, 449
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/118, 205
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 428
TYPE: PRT
ORGANISM: Homo sapiens
US-09-608-285A-3

Query Match 66.7%; Score 64; DB 4; Length 428;
Best Local Similarity 86.7%; Pred. No. 0.0028; 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2;

Qy 5 QETVGAIDLGASTQ 19
Db 192 QETVGTLDLGASTQ 206

RESULT 8
US-09-608-285A-7
Sequence 7, Application US/09608285A
Patient No. 6335013
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
FILE REFERENCE: 28110/36570
CURRENT APPLICATION NUMBER: US/09/608, 285A
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/583, 231
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350, 836
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481, 238
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/370, 265
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: 09/557, 800
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481, 238
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/370, 265
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350, 836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273, 447

RESULT 7
US-09-608-285A-5
Sequence 5, Application US/09608285A
Patient No. 6335013
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
FILE REFERENCE: 28110/36570
CURRENT APPLICATION NUMBER: US/09/608, 285A
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/583, 231
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350, 836
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481, 238
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/370, 265
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: 09/557, 800
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481, 238
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/370, 265
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350, 836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273, 447

Query Match 66.7%; Score 64; DB 4; Length 428;
Best Local Similarity 86.7%; Pred. No. 0.0028; 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2;

Qy 5 QETVGAIDLGASTQ 19
Db 192 QETVGTLDLGASTQ 206

RESULT 9
US-09-240-639-6
; Sequence 6, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240, 639
; CURRENT FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-240-639-6

RESULT 10
US-09-240-639-9
; Sequence 9, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauft, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240, 639
; CURRENT FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-240-639-9

Query Match 66.7%; Score 64; DB 4; Length 428;
Best Local Similarity 86.7%; Pred. No. 0.0028; Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 192 QETVGTLDLGCASTQ 206

RESULT 11
US-09-350-836B-3
; Sequence 9, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
; APPLICANT: Frischauft, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240, 639
; CURRENT FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-240-639-9

Query Match 66.7%; Score 64; DB 4; Length 428;
Best Local Similarity 86.7%; Pred. No. 0.0028; Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 192 QETVGTLDLGCASTQ 206

RESULT 12
US-09-350-836B-5
; Sequence 5, Application US/09350836B
; Patent No. 6387645
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulerio, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/09/350, 836B
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273, 447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/7118, 205
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/122, 449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244, 444
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-350-836B-5

Query Match 66.7%; Score 64; DB 4; Length 428;
Best Local Similarity 86.7%; Pred. No. 0.0028; Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 192 QETVGTLDLGCASTQ 206

RESULT 13
US-09-350-836B-7
; Sequence 7, Application US/09350836B
; Patent No. 6387645
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulerio, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/09/350, 836B
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273, 447
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-350-836B-7

Query Match 66.7%; Score 64; DB 4; Length 428;
Best Local Similarity 86.7%; Pred. No. 0.0028; Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 192 QETVGTLDLGCASTQ 206

PRIOR FILING DATE: 1999-03-19

PRIOR APPLICATION NUMBER: 09/118, 205

PRIOR FILING DATE: 1998-07-16

PRIOR APPLICATION NUMBER: 09/122, 449

PRIOR FILING DATE: 1998-07-24

PRIOR APPLICATION NUMBER: 09/244, 444

PRIOR FILING DATE: 1998-02-04

NUMBER OF SEQ ID NOS.: 23

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 7

LENGTH: 428

TYPE: PRT

ORGANISM: Homo sapiens

US-09-350-836B-7

Query Match 66.7%; Score 64; DB 4; Length 428;

Best Local Similarity 86.7%; Pred. No. 0.0028; Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 QETVGYALDGGASTQ 19

Db 192 QETVGYALDGGASTQ 206

RESULT 14

US-09-370-265-3

Sequence 3, Application US/09370265

Patent No. 644771

GENERAL INFORMATION:

APPLICANT: Ford, John

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE

TITLE OF INVENTION: POLYPEPTIDES

FILE REFERENCE: 2811/35908

CURRENT APPLICATION NUMBER: US/09/370, 265

CURRENt FILING DATE: 1999-08-09

EARLIER APPLICATION NUMBER: PCT/US99/16180

EARLIER FILING DATE: 1999-07-16

EARLIER APPLICATION NUMBER: 09/350, 836

EARLIER FILING DATE: 1998-07-09

EARLIER APPLICATION NUMBER: 09/273, 447

EARLIER FILING DATE: 1999-03-19

EARLIER APPLICATION NUMBER: 09/244, 444

EARLIER FILING DATE: 1999-02-04

EARLIER APPLICATION NUMBER: 09/122, 449

EARLIER FILING DATE: 1998-07-24

EARLIER APPLICATION NUMBER: 09/118, 205

EARLIER FILING DATE: 1998-07-16

NUMBER OF SEQ ID NOS.: 37

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: 428

TYPE: PRT

ORGANISM: Homo sapiens

US-09-370-265-3

Query Match 66.7%; Score 64; DB 4; Length 428;

Best Local Similarity 86.7%; Pred. No. 0.0028; Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 QETVGYALDGGASTQ 19

Db 192 QETVGYALDGGASTQ 206

RESULT 15

US-09-370-265-5

Sequence 5, Application US/09370265

Patent No. 644771

GENERAL INFORMATION:

APPLICANT: Ford, John

APPLICANT: Mulero, Julio

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE

TITLE OF INVENTION: POLYPEPTIDES

FILE REFERENCE: 2811/35908

CURRENT APPLICATION NUMBER: US/09/370, 265

CURRENt FILING DATE: 1998-08-09

EARLIER APPLICATION NUMBER: PCT/US99/16180

EARLIER FILING DATE: 1999-07-16

EARLIER APPLICATION NUMBER: 09/350, 836

EARLIER FILING DATE: 1998-07-09

EARLIER APPLICATION NUMBER: 09/273, 447

EARLIER FILING DATE: 1999-03-19

EARLIER APPLICATION NUMBER: 09/244, 444

EARLIER FILING DATE: 1999-02-04

EARLIER APPLICATION NUMBER: 09/122, 449

EARLIER FILING DATE: 1998-07-24

EARLIER APPLICATION NUMBER: 09/118, 205

EARLIER FILING DATE: 1998-07-16

NUMBER OF SEQ ID NOS.: 37

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: 428

TYPE: PRT

ORGANISM: Homo sapiens

US-09-370-265-3

Query Match 66.7%; Score 64; DB 4; Length 428;

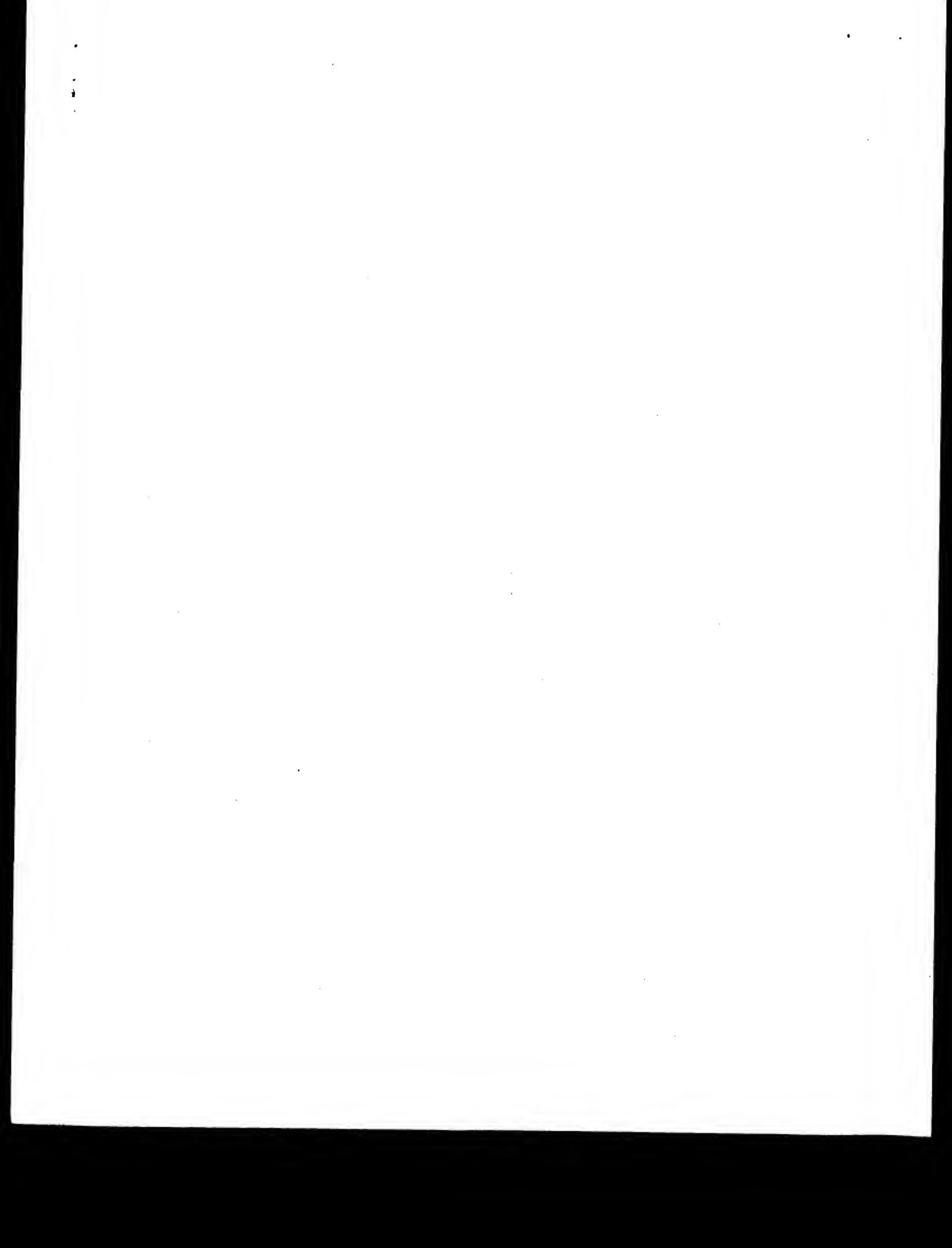
Best Local Similarity 86.7%; Pred. No. 0.0028; Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 QETVGYALDGGASTQ 19

Db 192 QETVGYALDGGASTQ 206

Search completed: February 11, 2003, 18:40:39

Job time : 32 secs



Query Match ; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
; US-09-835-147-6

Query Match ; Best Local Similarity 78.1%; Score 75; DB 10; Length 454;
; Matches 14; Conservative 73.7%; Pred. No. 4.4e-05; 4; Mismatches 1; Indels 0; Gaps 0;
; SEQ ID NO 1
; Qy 1 KSDIQETYGALDGGASTQ 19
; Db 180 ETNNQETFGALDDGAGSTQ 198

RESULT 3

CURRENT APPLICATION NUMBER: US/09/835,147
; Sequence 30 Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Majluszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimbel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
; US-09-835-147-27

Query Match ; Best Local Similarity 78.1%; Score 75; DB 10; Length 464;
; Matches 14; Conservative 73.7%; Pred. No. 4.5e-05; 4; Mismatches 1; Indels 0; Gaps 0;
; SEQ ID NO 1
; Qy 1 KSDIQETYGALDGGASTQ 19
; Db 190 ETNNQETFGALDDGAGSTQ 208

RESULT 5

US-09-835-147-29

Query Match ; Best Local Similarity 78.1%; Score 75; DB 10; Length 464;
; Matches 14; Conservative 73.7%; Pred. No. 4.5e-05; 4; Mismatches 1; Indels 0; Gaps 0;
; SEQ ID NO 29
; Qy 1 KSDIQETYGALDGGASTQ 19
; Db 190 ETNNQETFGALDDGAGSTQ 208

Query Match ; Best Local Similarity 78.1%; Score 75; DB 10; Length 463;
; Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
; SEQ ID NO 29
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
; US-09-835 147-30

Query Match ; Best Local Similarity 78.1%; Score 75; DB 10; Length 463;
; Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
; SEQ ID NO 29
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
; US-09-835 147-29

Query Match ; Best Local Similarity 78.1%; Score 75; DB 10; Length 473;
; Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
; SEQ ID NO 29
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
; US-09-835 147-29

Query Match ; Best Local Similarity 78.1%; Score 75; DB 10; Length 473;
; Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
; SEQ ID NO 29
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
; US-09-835 147-29

RESULT 4

US-09-835-147-27

Query Match ; Sequence 27 Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; Qy 1 KSDIQETYGALDGGASTQ 19
; Db 189 ETNNQETFGALDDGAGSTQ 207

RESULT 6 :::::::::::::::::::: 217
 Db 199 ETNNQETFGALDGGASTQ 217
 ; OTHER INFORMATION: Description of Artificial Sequence: Fusion
 ; OTHER INFORMATION: construct of human CD39
 US-09-835-147-3
 ; Sequence 28, Application US/09835147
 ; Patent No. US20020002277A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Maliszewski, Charles R.
 ; APPLICANT: Gayle III, Richard B.
 ; APPLICANT: Price, Virginia L.
 ; APPLICANT: Gimpel, Steven D.
 TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
 FILE REFERENCE: 2879-US
 CURRENT APPLICATION NUMBER: US/09/835, 147
 CURRENT FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: US 60/104, 585
 PRIOR FILING DATE: 1998-10-16
 PRIOR APPLICATION NUMBER: US 60/107, 466
 PRIOR FILING DATE: 1998-11-06
 PRIOR APPLICATION NUMBER: US 60/149, 010
 PRIOR FILING DATE: 1999-08-13
 PRIOR APPLICATION NUMBER: PCT/US99/22955
 PRIOR FILING DATE: 1999-10-13
 NUMBER OF SEQ ID NOS: 31
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 28
 LENGTH: 474
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Fusion
 OTHER INFORMATION: construct of human CD39
 US-09-835-147-28

Query Match 78.1%; Score 75; DB 10; Length 474;
 Best Local Similarity 73.7%; Pred. No. 4.6e-05; Matches 14; Conservatve 4; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

RESULT 7
 US-09-835-147-3
 Sequence 3, Application US/09835147
 ; Patent No. US20020002277A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gayle III, Richard B.
 ; APPLICANT: Gimpel, Steven D.
 ; APPLICANT: Price, Virginia L.
 ; APPLICANT: Maliszewski, Charles R.
 TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
 FILE REFERENCE: 2879-US
 CURRENT APPLICATION NUMBER: US/09/835, 147
 CURRENT FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: US 60/104, 585
 PRIOR FILING DATE: 1998-10-16
 PRIOR APPLICATION NUMBER: US 60/107, 466
 PRIOR FILING DATE: 1998-11-06
 PRIOR APPLICATION NUMBER: US 60/149, 010
 PRIOR FILING DATE: 1999-08-13
 PRIOR APPLICATION NUMBER: PCT/US99/22955
 PRIOR FILING DATE: 1999-10-13
 NUMBER OF SEQ ID NOS: 31
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 4
 LENGTH: 476
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Fusion
 OTHER INFORMATION: construct of human CD39
 NAME/KEY: VARIANT
 LOCATION: (39)
 OTHER INFORMATION: Any amino acid, preferably Cys or Ser

US-09-835-147-4

Query Match 78.1%; Score 75; DB 10; Length 476;
 Best Local Similarity 73.7%; Pred. No. 4.6e-05; Matches 14; Conservatve 4; Mismatches 1; Indels 0; Gaps 0;

Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

RESULT 8
 US-09-835-147-4
 Sequence 4, Application US/09835147
 ; Patent No. US20020002277A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Maliszewski, Charles R.
 ; APPLICANT: Gayle III, Richard B.
 ; APPLICANT: Price, Virginia L.
 ; APPLICANT: Gimpel, Steven D.
 TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
 FILE REFERENCE: 2879-US
 CURRENT APPLICATION NUMBER: US/09/835, 147
 CURRENT FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: US 60/104, 585
 PRIOR FILING DATE: 1998-11-06
 PRIOR APPLICATION NUMBER: US 60/149, 010
 PRIOR FILING DATE: 1999-08-13
 PRIOR APPLICATION NUMBER: PCT/US99/22955
 PRIOR FILING DATE: 1999-10-13
 NUMBER OF SEQ ID NOS: 31
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 4
 LENGTH: 476
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Fusion
 OTHER INFORMATION: construct of human CD39
 NAME/KEY: VARIANT
 LOCATION: (39)
 OTHER INFORMATION: Any amino acid, preferably Cys or Ser

US-09-835-147-4

Query Match 78.1%; Score 75; DB 10; Length 476;
 Best Local Similarity 73.7%; Pred. No. 4.6e-05; Matches 14; Conservatve 4; Mismatches 1; Indels 0; Gaps 0;

Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

RESULT 9
 US-09-835-147-8
 Sequence 8, Application US/09835147
 ; Patent No. US20020002277A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Maliszewski, Charles R.
 ; APPLICANT: Gayle III, Richard B.
 ; APPLICANT: Price, Virginia L.
 ; APPLICANT: Gimpel, Steven D.
 TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
 FILE REFERENCE: 2879-US
 CURRENT APPLICATION NUMBER: US/09/835, 147
 CURRENT FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: US 60/104, 585
 PRIOR FILING DATE: 1998-10-16
 NUMBER OF SEQ ID NOS: 31
 SOFTWARE: Patentin ver. 2.0
 LENGTH: 476
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:

; - PRIORITY FILING DATE: 1998-11-05
; PRIORITY APPLICATION NUMBER: US 60/149,010
; PRIORITY FILING DATE: 1999-08-13
; PRIORITY APPLICATION NUMBER: PCT/US99/22955
; PRIORITY FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
; US-09-835-147-8

Query Match 78.1%; Score 75; DB 10; Length 478;
Best Local Similarity 73.7%; Pred. No. 4.6e-05; Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KSDPQEYVGALDGAGSTQ 19
Db 204 ETNNQETFGALDGAGSTQ 222

RESULT 10

US-09-835-147-26

Sequence 25, Application US/09835147
Patent No. US20020002277A1
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimbel, Steven D.
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
FILE REFERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147
CURRNT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 26
LENGTH: 487
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion
OTHER INFORMATION: construct of human CD39
US-09-835-147-26

Query Match 78.1%; Score 75; DB 10; Length 487;
Best Local Similarity 73.7%; Pred. No. 4.7e-05; Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KSDPQEYVGALDGAGSTQ 19
Db 213 ETNNQETFGALDGAGSTQ 231

RESULT 11

US-10-092-063-38

Sequence 38, Application US/10092063
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio

Query Match 78.1%; Score 75; DB 10; Length 510;
Best Local Similarity 73.7%; Pred. No. 5e-05; Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KSDPQEYVGALDGAGSTQ 19
Db 202 ETNNQETFGALDGAGSTQ 220

RESULT 12

US-09-835-147-2

Sequence 2, Application US/09835147
Patent No. US20020002277A1
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimbel, Steven D.
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
FILE REFERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147
CURRNT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 510
TYPE: PRT
ORGANISM: Homo sapiens
US-09-835-147-2

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RESULT 13 ; Patent No. US20020173005A1
US-09-374-586-1 ; GENERAL INFORMATION:
; Sequence 1, Application US/09374586
; Patent No. US2002013889A1
; GENERAL INFORMATION:
; APPLICANT: Pinsky, David J.
; TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
; TITLE OF INVENTION: ISCHEMIC DISORDERS
; FILE REFERENCE: 05/5/59167
; CURRENT APPLICATION NUMBER: US/09/374, 586
; CURRENT FILING DATE: 1999-08-13
; CURRENT FILING DATE: 2002-03-05
; SEQ_ID NO: 1
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; LENGTH: 510
; TYPE: PRT
; ORGANISM: HOMO-SAPIEN
; US-09-374-586-1

Query Match 78.1%; Score 75; DB 10; Length 510;
Best Local Similarity 73.7%; Pred. No. 5e-05; Mismatches 4; Indels 1; Gaps 0;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KSDQPOETGALDGGASTQ 19
Db 202 ETNNQETGRALDGGASTQ 220

; SEQ_ID NO: 1
; LENGTH: 510
; TYPE: PRT
; ORGANISM: HOMO-SAPIEN
; US-09-374-586-1

RESULT 14
US-10-092-063-25 ; Patent No. US/10092063
; Sequence 25, Application US/10092063
; Patent No. US20020173005A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/10/092, 063
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/370, 265
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350, 836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/373, 447
; PRIOR FILING DATE: 1999-03-19
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244, 444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/350, 836
; PRIOR FILING DATE: 1999-07-24
; PRIOR APPLICATION NUMBER: 09/118, 205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ_ID NO: 3
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-092-063-3

Query Match 66.7%; Score 64; DB 9; Length 428;
Best Local Similarity 86.7%; Pred. No. 0.0029; Mismatches 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 QETYGAIDLGASTQ 19
Db 192 QETVGTIDLGASTQ 206

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Job time : 13 secs

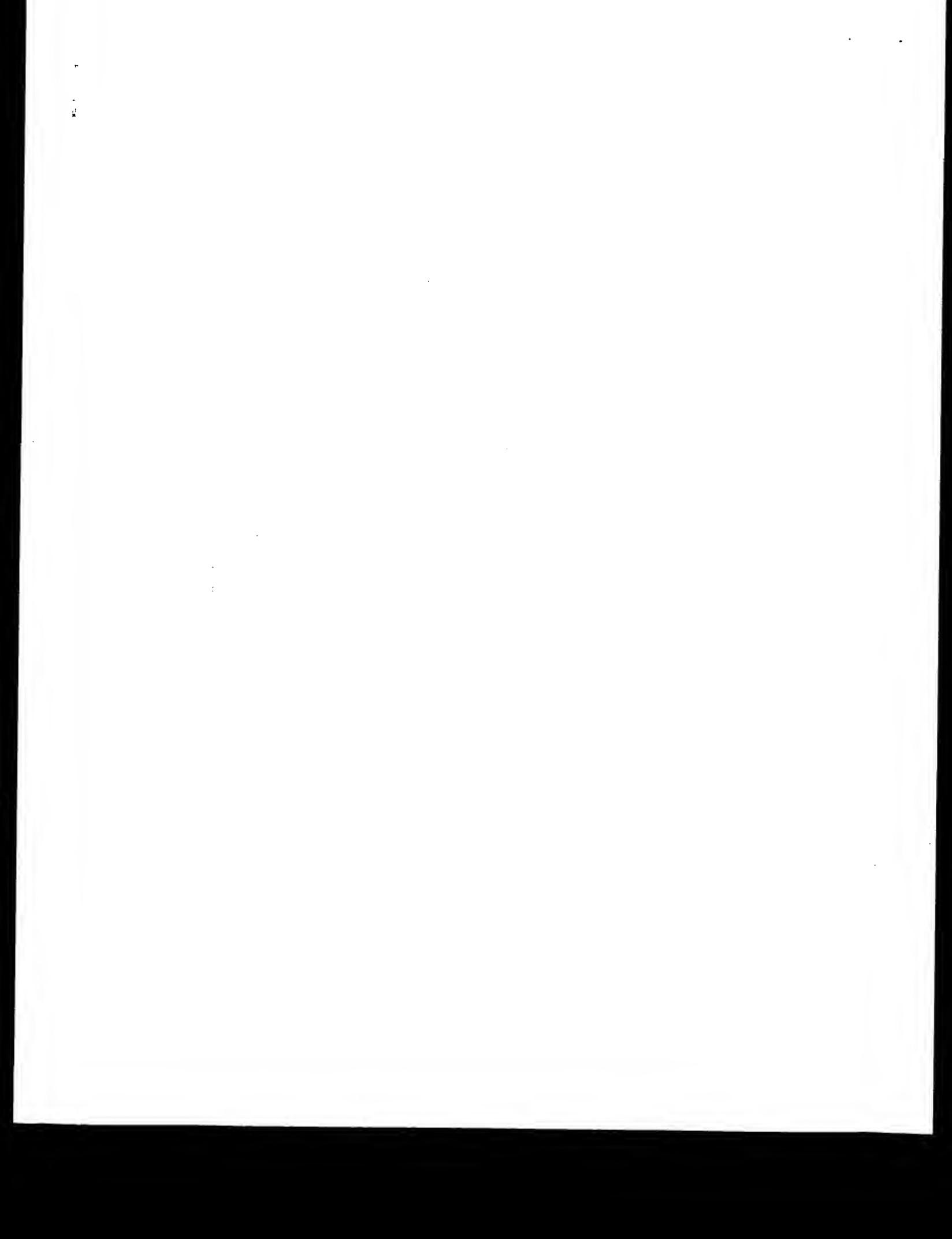
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; US-10-092-063-25

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Best Local Similarity 86.7%; Pred. No. 0.0027; Mismatches 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 QETYGAIDLGASTQ 19
Db 192 QETVGTIDLGASTQ 206

; LENGTH: 405
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-092-063-25

RESULT 15
US-10-092-063-3 ; Sequence 3, Application US/10092063
; Sequence 3, Application US/10092063
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OM protein - protein search, using sw model

Run on: February 11, 2003, 18:37:47 ; Search time 354 seconds
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Title: US-09-781-796B-7
 Perfect score: 1
 Sequence: KSDTQFVYGAIDLGGASQ 19

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 25: /cgn2_6/podata/1/paa/US1011_COMB.pep:*
- 26: /cgn2_6/podata/1/paa/US1022_COMB.pep:*
- 27: /cgn2_6/podata/1/paa/US60_COMB.pep:*

RESULT 1
 US-09-781-796B-7
 Sequence 7, Application US/09781796B
 GENERAL INFORMATION:
 APPLICANT: BEAUDOIN, Adrien R.
 APPLICANT: SVIGNY, Jean
 APPLICANT: BACH, Fritz H.
 APPLICANT: ROBSON, Simon
 TITLE OF INVENTION: ATP-DIPHOSPHORYLASES, PROCESS OF PURIFICATION
 TITLE OF INVENTION: THREEFOLD AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
 TITLE OF INVENTION: TECHNOLOGY
 FILE REFERENCE: 920333.90019
 CURRENT APPLICATION NUMBER: US/09/781,796B
 CURRENT FILING DATE: 2001-02-12
 PRIOR APPLICATION NUMBER: 08/419,204
 PRIOR FILING DATE: 1995-04-10
 PRIOR APPLICATION NUMBER: CA96/00223
 PRIOR FILING DATE: 1995-04-10
 PRIOR APPLICATION NUMBER: 08/930,921
 PRIOR FILING DATE: 1998-02-01
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: PatentIn Ver. 2.1
 SBO ID NO: 7
 LENGTH: 19
 TYPE: PRT
 ORGANISM: Porcine
 US-09-781-796B-7

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	96	100.0	19	Sequence 7, Appli
2	82	85.4	16	Sequence 8, Appli
3	75	78.1	276	Sequence 30, Appli
4	75	78.1	439	Sequence 2, Appli
5	75	78.1	439	Sequence 2, Appli
6	75	78.1	454	Sequence 6, Appli

Query Match

100.0%; Score 96; DB 21; Length 19;

Reiser

Best Local Similarity 100.0%; Pred. No. 3.5e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
 US-09-781-796B-8
 ; Sequence 8, Application US/09781796B
 ; GENERAL INFORMATION:
 ; APPLICANT: BEAUDOIN, Adrien R.
 ; APPLICANT: SUIGNY, Jean
 ; APPLICANT: BACH, Fritz H.
 ; APPLICANT: ROBSON, Simon
 TITLE OF INVENTION: ATP DIPHOSPHORYLASES, PROCESS OF PURIFICATION
 TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
 FILE REFERENCE: 920333.9019
 CURRENT APPLICATION NUMBER: US/09781.796B
 CURRENT FILING DATE: 2001-03-12
 PRIORITY APPLICATION NUMBER: US/09415,204
 PRIORITY FILING DATE: 1995-04-10
 PRIORITY APPLICATION NUMBER: CA06/00223
 PRIORITY FILING DATE: 1996-04-10
 PRIORITY APPLICATION NUMBER: 08/930,921
 PRIOR FILING DATE: 1998-02-01
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 8
 LENGTH: 16
 TYPE: PRT
 ORGANISM: Human and bovine
 US-09-781-796B-8

RESULT 3
 US-09-558-630A-30
 ; Sequence 30, Application US/09558630A
 ; GENERAL INFORMATION:
 ; APPLICANT: MINZ, Liat et al.
 ; TITLE OF INVENTION: ALTERNATIVE SPLICE VARIANTS
 ; CURRENT APPLICATION NUMBER: US/09/558,630A
 ; CURRENT FILING DATE: 2000-04-26
 ; NUMBER OF SEQ ID NOS: 82
 ; SEQ ID NO 30
 ; LENGTH: 276
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-558-630A-30

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 Best Local Similarity 100.0%; Pred. No. 7.7e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KSDTQETYGALDGGA 16
 Db 1 KSDTQETYGALDGGA 16

RESULT 5
 US-09-374-586-2
 ; Sequence 2, Application US/09374586
 ; GENERAL INFORMATION:
 ; APPLICANT: PINSKY, David J.
 TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND
 FILE REFERENCE: 0575/59167
 CURRENT APPLICATION NUMBER: US/09/374,586
 CURRENT FILING DATE: 1999-08-13
 NUMBER OF SEQ ID NOS: 2
 SEQ ID NO 2
 LENGTH: 439
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-374-586-2

Query Match 78.1%; Score 75; DB 17; Length 439;
 Best Local Similarity 73.7%; Pred. No. 0.00075;
 Matches 14; Conservative 73.7%; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KSDTQETYGALDGGA 19
 Db 165 ETNNOETFGALDGGA 183

RESULT 6
 PCT-US99-22955-6
 ; Sequence 6, Application PCT/US99/22955
 ; GENERAL INFORMATION:
 ; APPLICANT: Malszecki, Charles R.
 ; APPLICANT: Gayle III, Richard B.
 ; APPLICANT: Price, Virginia L.
 ; APPLICANT: Gimpel, Steven D.
 ; APPLICANT: Immunex Corporation
 ; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
 ; FILE REFERENCE: 2879-WO
 ; CURRENT APPLICATION NUMBER: PCT/US99/22955
 ; CURRENT FILING DATE: 1999-10-13
 ; EARLIER APPLICATION NUMBER: US 60/104,585
 ; EARLIER FILING DATE: 1998-10-16
 ; EARLIER APPLICATION NUMBER: US 60/107,466
 ; EARLIER FILING DATE: 1998-11-06
 ; EARLIER APPLICATION NUMBER: US 60/149,010
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn Ver. 2.0

RESULT 4
 PCT-US00-22060-2

SEQ_ID NO 6 ;
SEQ LENGTH: 454 ;
TYPE: PRT ;
ORGANISM: Artificial Sequence
PCT-US99-22955-6

Query Match 78.1%; Score 75; DB 1; Length 454;
Best Local Similarity 73.7%; Pred. No. 0.00079; 4; Mismatches 1; Indels 0; Gaps 0;
Matches 14; Conservative 4; Other Information: Description of Artificial Sequence: Fusion
QY 1 KSDTQETYGALDGGSATQ 19
Db 180 ETNNQETFGALDGGSATQ 198

RESULT 7
US-09-807-660A-6
Sequence 6, Application US/09807660A
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Marcus, Aaron J.
; APPLICANT: ImmuneX Corporation
; APPLICANT: Cornell Research Foundation, Inc.
TITLE OF INVENTION: Methods of Inhibiting Platelet Activation and Recruitment
FILE REFERENCE: 23,495 PCT
CURRENT APPLICATION NUMBER: US/09807,660A
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 454
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial sequence: Fusion
US-09-807-660A-6
Query Match 78.1%; Score 75; DB 22; Length 454;
Best Local Similarity 73.7%; Pred. No. 0.00079; 4; Mismatches 1; Indels 0; Gaps 0;
Matches 14; Conservative 4; Other Information: Description of Artificial Sequence: Fusion
QY 1 KSDTQETYGALDGGSATQ 19
Db 180 ETNNQETFGALDGGSATQ 198

RESULT 8
US-09-835-147-6
Sequence 6, Application US/09835147
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimbel, Steven D.
; APPLICANT: ImmuneX Corporation
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
FILE REFERENCE: 2879-WO
CURRENT APPLICATION NUMBER: PCT/US99/22955
CURRENT FILING DATE: 1999-10-13
EARLIER APPLICATION NUMBER: US 60/104,585
EARLIER FILING DATE: 1998-10-16
EARLIER APPLICATION NUMBER: US 60/107,466
EARLIER FILING DATE: 1998-11-06
EARLIER APPLICATION NUMBER: US 60/149,010
EARLIER FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
LENGTH: 463
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion
PCT-US99-22955-30
Query Match 78.1%; Score 75; DB 1; Length 463;
Best Local Similarity 73.7%; Pred. No. 0.00081; 4; Mismatches 1; Indels 0; Gaps 0;
Matches 14; Conservative 4; Other Information: Description of Artificial Sequence: Fusion
QY 1 KSDTQETYGALDGGSATQ 19
Db 189 ETNNQETFGALDGGSATQ 207

RESULT 10
US-09-807-660A-30
Sequence 30, Application US/09807660A
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Marcus, Aaron J.
; APPLICANT: ImmuneX Corporation
; APPLICANT: Cornell Research Foundation, Inc.
TITLE OF INVENTION: Methods of Inhibiting Platelet Activation and Recruitment
FILE REFERENCE: 23,495 PCT

CURRENT APPLICATION NUMBER: US/09/807,660A
 CURRENT FILING DATE: 2001-04-16
 PRIOR APPLICATION NUMBER: US 60/104,585
 PRIOR FILING DATE: 1998-10-16
 PRIOR APPLICATION NUMBER: US 60/107,466
 PRIOR FILING DATE: 1998-11-06
 PRIOR APPLICATION NUMBER: US 60/149,010
 PRIOR FILING DATE: 1999-08-13
 NUMBER OF SEQ ID NOS: 31
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 30
 LENGTH: 463
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Fusion
 ; OTHER INFORMATION: construct of human CD39
 US-09-807-660A-30

Query Match 78.1%; Score 75; DB 22; Length 463;
 Best Local Similarity 73.7%; Pred. No. 0.00081;
 Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Qy I KSDTOETYGALDGGASTQ 19
 Db 189 ETNNQETFGALDGGASTQ 207

RESULT 11
 US-09-835-147-30
 Sequence 30; Application US/09835147
 GENERAL INFORMATION:
 APPLICANT: Maliszewski, Charles R.
 APPLICANT: Gayle III, Richard B.
 APPLICANT: Price, Virginia L.
 APPLICANT: Gimpel, Steven D.
 TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
 FILE REFERENCE: 2879-US
 CURRENT APPLICATION NUMBER: US/09/835,147
 CURRENT FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: US 60/104,585
 PRIOR FILING DATE: 1998-10-16
 PRIOR APPLICATION NUMBER: US 60/107,466
 PRIOR FILING DATE: 1998-11-06
 PRIOR APPLICATION NUMBER: US 60/149,010
 PRIOR FILING DATE: 1999-08-13
 PRIOR APPLICATION NUMBER: PCT/US99/22955
 PRIOR FILING DATE: 1999-10-13
 NUMBER OF SEQ ID NOS: 31
 SOFTWARE: PatentIn Ver. 2.0
 LENGTH: 463
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Fusion
 ; OTHER INFORMATION: construct of human CD39
 US-09-835-147-30

Query Match 78.1%; Score 75; DB 22; Length 463;
 Best Local Similarity 73.7%; Pred. No. 0.00081;
 Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Qy I KSDTOETYGALDGGASTQ 19
 Db 189 ETNNQETFGALDGGASTQ 207

RESULT 13
 US-09-807-660A-27
 Sequence 27; Application US/09807660A
 GENERAL INFORMATION:
 APPLICANT: Maliszewski, Charles R.
 APPLICANT: Gayle III, Richard B.
 APPLICANT: Marcus, Aaron J.
 APPLICANT: Immunex Corporation
 APPLICANT: Cornell Research Foundation, Inc.
 TITLE OF INVENTION: Methods of Inhibiting Platelet Activation and Recruitment
 FILE REFERENCE: 23-495 PCT
 CURRENT APPLICATION NUMBER: US/09/807,660A
 CURRENT FILING DATE: 2001-04-16
 PRIOR APPLICATION NUMBER: US 60/104,585
 PRIOR FILING DATE: 1998-10-16
 PRIOR APPLICATION NUMBER: US 60/107,466
 PRIOR FILING DATE: 1998-11-06
 PRIOR APPLICATION NUMBER: US 60/149,010
 PRIOR FILING DATE: 1999-08-13
 NUMBER OF SEQ ID NOS: 31
 SOFTWARE: PatentIn Ver. 2.0
 LENGTH: 464
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Fusion
 ; OTHER INFORMATION: construct of human CD39
 US-09-807-660A-27

Query Match 78.1%; Score 75; DB 22; Length 464;
 Best Local Similarity 73.7%; Pred. No. 0.00081;
 Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Qy I KSDTOETYGALDGGASTQ 19
 Db 190 ETNNQETFGALDGGASTQ 208

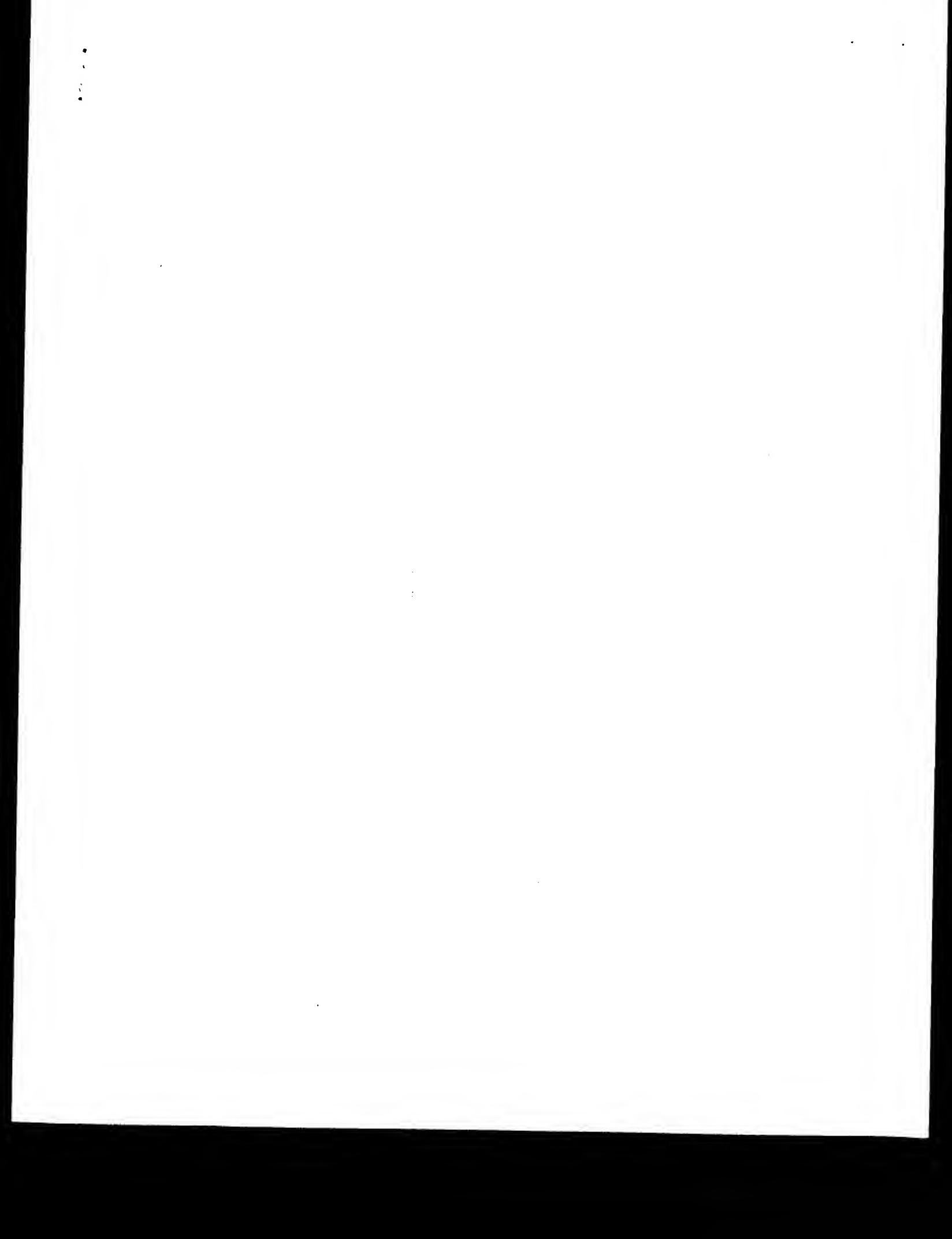
RESULT 14
US-09-835-147-27
Sequence 27; Application US/09835147
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
FILE REFERENCE: 2879-US
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 27
LENGTH: 464
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial sequence: Fusion
OTHER INFORMATION: construct of human CD39
US-09-835-147-27

Query Match 78.1%; Score 75; DB 22; Length 464;
Best Local Similarity 73.7%; Pred. No. 0.0001; Mismatches 1; Indels 0; Gaps 0;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KSDPQETYGALDLGGASTQ 19
Db 199 ETNNQETFGALDLGGASTQ 217

RESULT 15
PCT-US99-22955-29
Sequence 29; Application PC/TUS9922955
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
APPLICANT: Immunex Corporation
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
FILE REFERENCE: 2879-WO
CURRENT APPLICATION NUMBER: PCT/US99/22955
CURRENT FILING DATE: 1999-10-13
EARLIER APPLICATION NUMBER: US 60/104,585
EARLIER FILING DATE: 1998-10-16
EARLIER APPLICATION NUMBER: US 60/107,466
EARLIER FILING DATE: 1998-11-06
EARLIER APPLICATION NUMBER: US 60/149,010
EARLIER FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 29
LENGTH: 473
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion
OTHER INFORMATION: construct of human CD39
PCT-US99-22955-29

Query Match 78.1%; Score 75; DB 1; Length 473;
Best Local Similarity 73.7%; Pred. No. 0.0003;



Db 202 ETNNQETFGALDLGGASTQ 220 US-10-049-420-2

RESULT 3 Query Match Best Local Similarity 78.1%; Score 75; DB 6; Length 439; SEQ ID NO: 59000 Pred. No. 0.00021; Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

; Sequence 59000, Application US/09724676 GENERAL INFORMATION:

; APPLICANT: Compugen LTD TITLE OF INVENTION: Variants of alternative splicing

; CURRENT APPLICATION NUMBER: US/09/724,676 CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222 SOFTWARE: PatentIn version 3.2

; SEQ ID NO 59000 LENGTH: 283 TYPE: PRT

; ORGANISM: Homo sapiens US-09-724-676-59000

Query Match Best Local Similarity 78.1%; Score 75; DB 5; Length 283; Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDTQETYGALDLGGASTQ 19 Db 209 ETNNQETFGALDLGGASTQ 227

RESULT 4 US-09-724-676A-59000

; Sequence 59000, Application US/09724676A GENERAL INFORMATION:

; APPLICANT: Compugen LTD TITLE OF INVENTION: Variants of alternative splicing

; CURRENT APPLICATION NUMBER: US/09724,676A CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222 SOFTWARE: PatentIn version 3.2 SEQ ID NO 59000 LENGTH: 283 TYPE: PRT

; ORGANISM: Homo sapiens US-09-724-676A-59000

Query Match Best Local Similarity 78.1%; Score 75; DB 5; Length 283; Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDTQETYGALDLGGASTQ 19 Db 209 ETNNQETFGALDLGGASTQ 227

RESULT 5 US-10-049-420-2

; Sequence 2, Application US/10049420 GENERAL INFORMATION:

; APPLICANT: Flisiky, David J. TITLE OF INVENTION: CD39/ACTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND FILE REFERENCE: 0575/59167 CURRENT APPLICATION NUMBER: US/10/049,420 PRIOR FILING DATE: 2002-02-06 PRIOR APPLICATION NUMBER: US/09/374,586 NUMBER OF SEQ ID NOS: 2 SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 2 LENGTH: 439 TYPE: PRT

; ORGANISM: Homo sapiens

Query Match Best Local Similarity 78.1%; Score 75; DB 5; Length 439; SEQ ID NO 59000 Pred. No. 0.00021; Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDTQETYGALDLGGASTQ 19 Db 165 ETNNQETFGALDLGGASTQ 183

RESULT 6 US-09-835-147A-6

; Sequence 6, Application US/9835147A GENERAL INFORMATION:

; APPLICANT: Maliszewski, Charles R. APPLICANT: Gayle III, Richard B. APPLICANT: Price, Virginia L. TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT FILE REFERENCE: 2879-US CURRENT APPLICATION NUMBER: US/09/835,147A CURRENT FILING DATE: 2001-04-13

; NUMBER OF SEQ ID NOS: 37 SOFTWARE: PatentIn version 3.1 SEQ ID NO 6 LENGTH: 454

TYPE: PRT

; ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Fusion construct of human CD39

US-09-835-147A-6

Query Match Best Local Similarity 78.1%; Score 75; DB 5; Length 454; Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSDTQETYGALDLGGASTQ 19 Db 180 ETNNQETFGALDLGGASTQ 198

RESULT 7 US-09-835-147A-30

; Sequence 30, Application US/09835147A GENERAL INFORMATION:

; APPLICANT: Maliszewski, Charles R. APPLICANT: Gayle III, Richard B. APPLICANT: Price, Virginia L.

; APPLICANT: Gimpel, Steven D. TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT FILE REFERENCE: 2879-US CURRENT APPLICATION NUMBER: US/09/835,147A CURRENT FILING DATE: 2001-04-13

PRIOR APPLICATION NUMBER: US/60/104,585 PRIOR FILING DATE: 1998-10-16 PRIOR APPLICATION NUMBER: US 60/107,466 PRIOR FILING DATE: 1998-11-06 PRIOR APPLICATION NUMBER: US 60/149,010 PRIOR FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: PCT/US99/22955 PRIOR FILING DATE: 1999-10-13

PRIOR APPLICATION NUMBER: PCT/US99/22955 NUMBER OF SEQ ID NOS: 37 SOFTWARE: PatentIn version 3.1 SEQ ID NO 30

us-09-781-796b-7.rapn

LENGTH: 463
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Fusion construct of human CD39
 US-09-835-147A-30

Query Match 78.1%; Score 75; DB 5; Length 463;
 Best Local Similarity 73.7%; Pred. No. 0.00022; 4; Mismatches 1; Indels 0; Gaps 0;
 Matches 14; Conservative 4; Prior Filing Date: 1998-10-13

RESULT 8
 US-09-835-147A-27
 Sequence 27, Application US/09835147A
 GENERAL INFORMATION:
 APPLICANT: Maliszewski, Charles R.
 APPLICANT: Gayle III, Richard B.
 APPLICANT: Price, Virginia L.
 APPLICANT: Gimpel, Steven D.
 TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
 FILE REFERENCE: 2879-US
 CURRENT APPLICATION NUMBER: US/09/835,147A
 CURRENT FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: US 60/104,585
 PRIOR FILING DATE: 1998-10-16
 PRIOR APPLICATION NUMBER: US 60/107,466
 PRIOR FILING DATE: 1998-11-06
 PRIOR APPLICATION NUMBER: US 60/149,010
 PRIOR FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: PCT/US99/22955
 PRIOR FILING DATE: 1999-10-13
 NUMBER OF SEQ ID NOS: 37
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 27
 LENGTH: 464
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: Fusion construct of human CD39
 US-09-835-147A-27

Query Match 78.1%; Score 75; DB 5; Length 464;
 Best Local Similarity 73.7%; Pred. No. 0.00022; 4; Mismatches 1; Indels 0; Gaps 0;
 Matches 14; Conservative 4; Prior Filing Date: 1998-10-13

RESULT 9
 US-09-835-147A-29
 Sequence 29, Application US/09835147A
 GENERAL INFORMATION:
 APPLICANT: Maliszewski, Charles R.
 APPLICANT: Gayle III, Richard B.
 APPLICANT: Price, Virginia L.
 APPLICANT: Gimpel, Steven D.
 TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
 FILE REFERENCE: 2879-US
 CURRENT APPLICATION NUMBER: US/09/835,147A
 CURRENT FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: US 60/104,585
 PRIOR FILING DATE: 1998-10-16
 PRIOR APPLICATION NUMBER: US 60/107,466
 PRIOR FILING DATE: 1998-11-06
 PRIOR APPLICATION NUMBER: US 60/149,010
 PRIOR FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: PCT/US99/22955
 PRIOR FILING DATE: 1999-10-13
 NUMBER OF SEQ ID NOS: 37
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 28
 LENGTH: 474
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: Fusion construct of human CD39
 US-09-835-147A-28

Query Match 78.1%; Score 75; DB 5; Length 474;
 Best Local Similarity 73.7%; Pred. No. 0.00023; 4; Mismatches 1; Indels 0; Gaps 0;
 Matches 14; Conservative 4; Prior Filing Date: 1998-10-13

RESULT 10
 US-09-835-147A-29
 Sequence 28, Application US/09835147A
 GENERAL INFORMATION:
 APPLICANT: Maliszewski, Charles R.
 APPLICANT: Gayle III, Richard B.
 APPLICANT: Price, Virginia L.
 APPLICANT: Gimpel, Steven D.
 TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
 FILE REFERENCE: 2879-US
 CURRENT APPLICATION NUMBER: US/09/835,147A
 CURRENT FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: US 60/104,585
 PRIOR FILING DATE: 1998-10-16
 PRIOR APPLICATION NUMBER: US 60/107,466
 PRIOR FILING DATE: 1998-11-06
 PRIOR APPLICATION NUMBER: US 60/149,010
 PRIOR FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: PCT/US99/22955
 PRIOR FILING DATE: 1999-10-13
 NUMBER OF SEQ ID NOS: 37
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 28
 LENGTH: 474
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: Fusion construct of human CD39
 US-09-835-147A-28

Query Match 78.1%; Score 75; DB 5; Length 474;
 Best Local Similarity 73.7%; Pred. No. 0.00023; 4; Mismatches 1; Indels 0; Gaps 0;
 Matches 14; Conservative 4; Prior Filing Date: 1998-10-13

RESULT 11
 US-09-835-147A-33
 Sequence 3, Application US/09835147A
 GENERAL INFORMATION:
 APPLICANT: Maliszewski, Charles R.
 APPLICANT: Gayle III, Richard B.
 APPLICANT: Price, Virginia L.
 APPLICANT: Gimpel, Steven D.
 TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
 FILE REFERENCE: 2879-US
 CURRENT APPLICATION NUMBER: US/09/835,147A
 CURRENT FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: US 60/104,585
 PRIOR FILING DATE: 1998-10-16
 PRIOR APPLICATION NUMBER: US 60/107,466
 PRIOR FILING DATE: 1998-11-06
 PRIOR APPLICATION NUMBER: US 60/149,010
 PRIOR FILING DATE: 1998-08-13

RESULT 15

US-09-835-147A-2

; Sequence 2, Application US/09835147A.

; GENERAL INFORMATION:

; APPLICANT: Maliszewski, Charles R.

; APPLICANT: Gayle III, Richard B.

; APPLICANT: Gimpel, Steven D.

; APPLICANT: Price, Virginia L.

; TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT

; CURRENT APPLICATION NUMBER: US/09/835,147A

; CURRENT FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: US 60/104,585

; PRIOR FILING DATE: 1998-10-16

; PRIOR APPLICATION NUMBER: US 60/107,466

; PRIOR FILING DATE: 1998-11-06

; PRIOR APPLICATION NUMBER: US 60/149,010

; PRIOR FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: PCT/US99/22055

; PRIOR FILING DATE: 1999-10-13

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 510

; TYPE: PRT

; ORGANISM: Homo sapiens

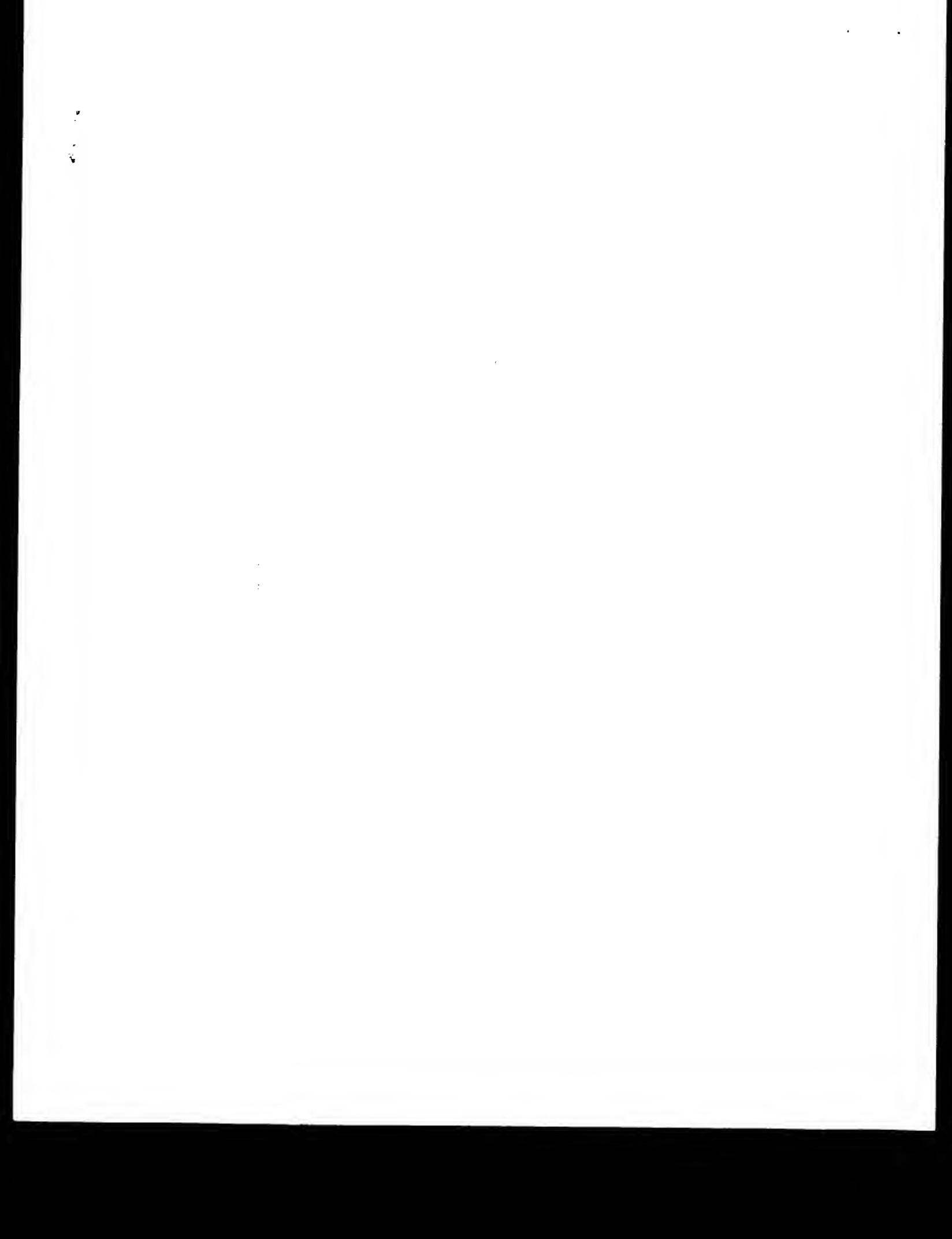
; US-09-835-147A-2

Query Match 78.1%; Score 75; DB 5; Length 510;
Best Local Similarity 73.7%; Pred. No. 0; 0.0024; Length 510;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KSDTQEYGAALDGGASTQ 19

Db 202 ETNNQETFGAALDGGASTQ 220

Search completed: February 11, 2003, 18:47:06
Job time : 20 secs



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Gencore version 5.1.3

OM protein - protein search, using SW model

Run on: February 11, 2003, 18:35:31 ; search time 16 Seconds
(without alignments)
114.160 Million cell updates/sec

Title: US-09-781-796B-7

Perfect score: 96

Sequence: 1 KSDTQETYGALDGGASTQ 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 9613422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. 1s is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	75	78.1	510	2	I56242 lymphoid cell acti
2	62	64.6	44	2	S63501 apyrase (EC 3.6.1).
3	53	55.2	1052	2	T04439 hypothetical prote
4	52	54.2	630	2	S50463 probable guanosine
5	51	53.1	556	2	T39109 hypothetical prote
6	50	52.1	557	2	T16696 hypothetical prote
7	49	51.0	483	2	D86276 probable nucleotid
8	47	49.0	124	1	FAD022 probable nucleotid
9	45.5	48.4	572	2	T40556 hypothetical prote
10	44	45.8	263	2	C70741 hypothetical prote
11	44	45.8	377	2	S55605 hypothetical prote
12	44	45.8	405	2	E86276 nucleoside triphos
13	44	45.5	548859	2	S48859 probable nucleosid
14	44	45.8	4516	2	G84442 nuclear antigen EB
15	44	45.8	925	2	S27920 polymorphic outer
16	43	44.8	494	2	JC5096 transposase - fung
17	43	44.8	534	2	T04798 hypothetical prote
18	42	43.8	421	2	T04798 hypothetical prote
19	42	43.8	479	2	T23508 botulinum neurotox
20	41.5	43.8	293	2	H44644 iron-sulfur cluste
21	41	42.7	262	1	D69447 protein C48p10.9
22	41	42.7	416	2	A88109 apyrace (EC 3.6.1.
23	41	42.7	454	2	JC46116 propionyl coenzyme
24	41	42.7	470	2	A96286 propionyl-CoA carb
25	41	42.7	510	2	AH2297 transcription acti
26	41	42.7	510	2	AC3352 propionyl-CoA carb
27	41	42.7	519	2	A38073 transcription acti
28	41	42.7	677	2	transcription acti
29	40.5	42.2	809	2	F87458 conserved hypothet

ALIGNMENTS

RESULT 1

I56242 lymphoid cell activation antigen - human

N;Species: Homo sapiens (man)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C;Accession: I56242

R;Malinewski, C.R.; Delepesse, G.J.; Schoenborn, M.A.; Armitage, R.J.; Fanslow, W.C.

J; Immunol. 153: 3574-3583, 1994

A;Title: The CD39 lymphoid cell activation antigen. Molecular cloning and structural

A;Reference number: I56242; MUID:95015846; PMID:7930580

A;Accession: I56242

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-510 <rbs>

A;Cross-references: GB:S73813; NID:9765255; PIDN:AAB32152.1; PID:9765256

Query Match

78.1%; Score 75; DB 2; Length 510;

Best Local Similarity

73.7%; Pred. No. 9e-05;

Matches 14; Conservative

4; Mismatches 1; Indels 0; Gaps 0;

QY

1 KSDTQETYGALDGGASTQ 19

Db

202 ETNNQETFGALDGGASTQ 220

RESULT 1

S63501 apyrase (EC 3.6.1.5) - human (fragments)

N;Alternate names: ATP diphosphohydrolase

C;Species: Homo sapiens (man)

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997

C;Accession: S63501

R;Christofidis, S.; Papamarcaki, T.; Galaris, D.; Kellner, R.; Tsolis, O.

Bur. J. Biochem. 234: 66-74, 1995

A;Title: Purification and properties of human placental ATP diphosphohydrolase.

A;Reference number: S63501; MUID:96096723; PMID:8529670

A;Accession: S63501

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-3;4-8;9-13;14-20;21-30;31-44 <CHR>

C;Keywords: hydrolase

Query Match 64.6%; Score 62; DB 2; Length 44;

Best Local Similarity 85.7%; Pred. No. 0.001;

Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 ETYGALDGGASTQ 19

Db 28 DLYGALDGGASTQ 41

RESULT 3

30 40 41.7 425 2 H70456 nodulation competi

31 40 41.7 485 2 T34147 hypothetical prote

32 40 41.7 522 2 B71970 glutamic acid-rich

33 40 41.7 590 2 A40437 dimethylsulfoxide

34 40 41.7 808 2 E64914 hypothetical prote

35 40 41.7 828 2 F96555 glucose transport

36 40 41.7 884 2 A31928 multi-protein - C10 dinak-type molecule

37 39 41.1 463 1 I40661 tRNA Isopenicenylyl

38 39 40.6 227 2 B86703 tRNA Isopenicenylyl

39 39 40.6 294 2 G95075 tRNA Isopenicenylyl

40 39 40.6 311 2 D97945 xylose operon regul

41 39 40.6 315 2 F70203 protein kinase pkn

42 39 40.6 505 1 S77034 guanosine-diphosph

43 39 40.6 518 2 A4076 2 A87518 hypothetical prote

T04439 hypothetical protein T18B16_150 - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
 R;Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.; Bancroft, I.; Mewes, H.W.
 submitted to the Protein Sequence Database, April 1998
 A;Reference number: Z15359
 A;Accession: T04439
 A;Molecule type: DNA
 A;Residue: 1-1052 <BEV>
 A;Experimental source: cultivar Columbia; BAC clone T18B16
 A;Cross-references: EMBL:AL021687
 A;genetics:
 A;Map position: 4 118/3; 217/1; 295/3; 396/3; 531/2; 815/3
 A;Introns: 79/3; 110
 A;Note: T18B16.150

Query Match 55.2%; Score 53; DB 2; Length 1052;
 Best Local Similarity 76.9%; Pred. No. 1.2;
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 TYGALDIQCASTQ 19
 :|||||:|||||

Db 685 TFGALDQGSSLQ 697

RESULT 4

550463 hypothetical protein YER005w - Yeast (*Saccharomyces cerevisiae*)
 C;Species: *Saccharomyces cerevisiae*
 C;Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 19-Apr-2002
 C;Accession: S50463
 R;Dietrich, F.S.
 submitted to the EMBL Data Library, December 1994
 A;Description: The sequence of *S. cerevisiae* cosmids 9537, 9581, 9495, 9867, and lambda
 A;Reference number: S50433
 A;Accession: S50463
 A;Molecule type: DNA
 A;Residues: 1-630 <DEB>
 A;Cross-references: EMBL:U18778; NID:9603592; PID:9603597; GSPDB:GN00005; MIPS:YER005w
 A;Genetics:
 A;Gene: SGD:YND1; MIPS:YER005w
 A;Cross-references: SGD:S0000807
 A;Map position: 5R

Query Match 54.2%; Score 52; DB 2; Length 630;
 Best Local Similarity 69.2%; Pred. No. 0.99; Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 7 TFGALDIQCASTQ 19
 :|||||:|||||

Db 179 TFGALDQGASTQ 191

RESULT 5

T39109 probable guanosine-diphosphatase - fission yeast (*Schizosaccharomyces pombe*)
 C;Species: *Schizosaccharomyces pombe*
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C;Accession: T39109
 R;Barrell, B.G.; Roelandse, M.A.; Quail, M.; Seagar, K.; Harris, D.
 submitted to the EMBL Data Library, October 1999
 A;Reference number: 22828
 A;Accession: T39109
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-556 <BAR>
 A;Cross-references: EMBL:AU121741; PIDN:CA57338_1; GSPDB:GN00066; SPDB:SPAC824_08
 A;Experimental source: strain 972h-; cosmid c824
 C;Genetics:
 A;Gene: SPDB:SPAC824_08
 A;Map position: 1

Query Match 53.1%; Score 51; DB 2; Length 556;
 Best Local Similarity 62.5%; Pred. No. 1.3; Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 TOETYGALDIQCASTQ 19
 :|||||:|||||

Db 276 THSTVAVMDIGGASTQ 291

RESULT 6

T16696 hypothetical protein R07E4_A - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C;Accession: T16696
 R;Miller, N.
 submitted to the EMBL Data Library, October 1995
 A;Description: The sequence of *C. elegans* cosmid R07E4.
 A;Reference number: Z18561
 A;Accession: T16696
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-557 <ML>
 A;Cross-references: EMBL:U39652; NID:91049390; PID:91049394; PIDN:AAA80403_1; GSPB:R0
 A;Experimental source: strain Bristol N2
 A;Genetics:
 A;Gene: CESP:R07E4_4
 A;Introns: 39/1; 67/1; 145/2; 192/1; 244/3; 317/3; 451/3; 488/2

Query Match 52.1%; Score 50; DB 2; Length 557;
 Best Local Similarity 60.0%; Pred. No. 1.9; Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 QETYGALDIQCASTQ 19
 :|||||:|||||

Db 212 QKTYGMIQDGGSQ 226

RESULT 7

D86276 hypothetical protein F7A19_34 [imported] - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Accession: D86276
 R;Theologis, A.; Becker, J.R.; Palm, C.J.; Fedderspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, N.; Huijar, L.; Nature 408, 816-820, 2000
 Authors: Hunter, J.D.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Talloker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.;
 A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A;Reference number: A86141; NID:21016719; PMID:11130712
 A;Accession: D86276
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-483 <TPO>
 A;Cross-references: GB:AB005172; NID:95080801; PIDN:AD39311_1; GSPDB:GN00141
 A;Genetics:
 A;Map position: 1

Query Match 51.0%; Score 49; DB 2; Length 483;
 Best Local Similarity 55.6%; Pred. No. 2.4; Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 SDTQETYGALDIQCASTQ 19
 :|||||:|||||

Db 212 TDPLERGTGIVELGGASQ 229

RESULT 8
 FAD02
 profilin II - slime mold (*Dicyostelium discoideum*)
 C;Species: *Dicyostelium discoideum*
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 22-Jun-1999
 C;Accession: B53255; S18028
 R;Haugwitz, M.; Noegel, A.A.; Rieger, D.; Lottspeich, F.; Schleicher, M.
 J; Cell Sci. 100, 481-489, 1991
 A;Title: *Dicyostelium discoideum* contains two profilin isoforms that differ in structure
 A;Reference number: AS3255; MUID:9226170; PMID:1725525
 A;Accession: B53255
 A;Molecule type: mRNA
 A;Cross-references: EMBL:XG1580; NID:g7325; PIDN:CAA43780.1; PID:g7326
 A;Note: parts of this sequence, including the amino end of the mature protein, were cont
 C;Superfamily: profilin
 C;Keywords: actin binding; methylated amino acid
 F;102/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
 F;2-124/Product: Profilin II #status experimental <MAT>
 Query Match 49.0%; Score 47; DB 1; Length 124;
 Best Local Similarity 60.0%; Pred. No. 1;2;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 KSDPQPTGYGALDGG 15
 ||||:|||:
 Db 70 KSDTRSYAYGRLGG 84
 ||||:
 RESULT 9
 T40856
 probable nucleotide phosphatase - fission yeast (*Schizosaccharomyces pombe*)
 C;Species: *Schizosaccharomyces pombe* #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C;Accession: T40856
 R;Ramsperger, U.; Pohl, T.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, October 1999
 A;Reference number: Z21952
 A;Accession: T40856
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-572 <UR>
 A;Cross-references: EMBL:AL121783; PIDN:CAB57847.1; GSPDB:GN00068; SPDB:SPCC11E10.05C
 A;Experimental source: strain 972h-; cosmid c11E10
 C;Genetics:
 A;Gene: SPB:SPCC11E10.05C
 A;Map position: 3
 RESULT 10
 C70741
 hypothetical protein Rv1356c - *Mycobacterium tuberculosis* (strain H37RV)
 C;Species: *Mycobacterium tuberculosis*
 C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
 C;Accession: J70741
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feilwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
 A;Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
 A;Reference number: R70500; MUID:9825987; PMID:9634230
 A;Accession: C70741
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA

RESULT 11
 S55055
 hypothetical 41.9k protein (leuX-fecE intergenic region) - *Escherichia coli* (strain K
 N) #status predicted
 C;Species: *Escherichia coli* #sequence_revision 03-Nov-1995 #text_change 01-Mar-2002
 C;Accession: S55055; B65241
 R;Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
 Nucleic Acids Res. 23, 2105-2119, 1995
 A;Title: Analysis of the *Escherichia coli* genome VI: DNA sequence of the region from
 A;Reference number: S55054; MUID:95334362; PMID:7610040
 A;Accession: S55055
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-377 <UR>
 A;Cross-references: EMBL:U14003; NID:g1263172; PIDN:AAA97176.1; PID:g537121
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
 A.; Rose, D.J.; Maur, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A;Title: The complete genome sequence of *Escherichia coli* K-12.
 A;Reference number: A64720; MUID:97426617; PMID:9278503
 A;Accession: B65241
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-377 <BLAT>
 A;Cross-references: GB:AB000498; GB:U00096; NID:92367368; PIDN:AC77236.1; PID:g17907
 A;Experimental source: strain K-12, substrain MG1655
 C;Genetics:
 C;Gene: yjhC
 A;Map position: 3
 RESULT 12
 R86276
 hypothetical protein F14L17.1 - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
 C;Accession: E86276
 R;Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, N.F.; Hughes, B.; Huizar, L.; Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luens, J.S.; Maiti, R.; Marzia, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Salzberg, S.L.; Schwarz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tally, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Authors: Salzberg, S.L.; Schwarz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tally, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the Plant *Arabidopsis*.
 A;Reference number: A86141; MUID:21016719; PMID:11130712

RESULT 15
 A;Accession: E86767
 A;Status: preliminary
 A;Cross-references: GB:AE005172; NID:9726666; PIDN:AAF43924.1; GSPDB:GN00141
 C;Genetics:
 A;Map position: 1
 Query Match 45.8%; Score 44; DB 2; Length 405;
 Best Local Similarity 52.9%; Pred. No. 14; Mismatches 5; Indels 0; Gaps 0;
 Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
Qy 3 DPOETYGALDGGSQ 19
Db 131 DPLKTTGIVELGGASQ 147

RESULT 13
 548859
 nucleoside triphosphatase precursor, chromatin-associated - garden pea
 C;Species: *Psium sativum* (garden pea)
 C;Accession: M56147
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 29-Sep-1999
 R;Hsieh, H.L.; Tong, C.G.; Thomas, C.; Roux, S.J.
 Plant Mol. Biol. 30, 135-147, 1996
 A;Title: Light-modulated abundance of an mRNA encoding a calmodulin-regulated, chromatin-associated protein.
 A;Accession: S65141; MUID:96197404; PMID:8616230
 A;Molecule type: mRNA
 A;Residues: 1-455 <H2>
 A;Cross-references: EMBL:Z32743; NID:9563611; PIDN:CAA83655.1; PID:9563612
 C;Superfamily: nucleoside triphosphatase chromatin-associated
 C;Keywords: nucleus

Query Match 45.8%; Score 44; DB 2; Length 455;
 Best Local Similarity 57.1%; Pred. No. 16; Mismatches 2; Indels 0; Gaps 0;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 6 ERYGALDGGSQ 19
Db 189 KTVGVIDLGGSVQ 202

RESULT 14
 G84442
 probable nucleoside triphosphatase [imported] - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Accession: G84442
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shear, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Meissner, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A;Accession: G84442
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-156 <STO>
 A;Cross-references: GB:AE002093; NID:93461821; PIDN: AAC32915.1; GSPDB:GN00139
 A;Gene: Att92970
 A;Map position: 2

Query Match 45.8%; Score 44; DB 2; Length 516;
 Best Local Similarity 52.9%; Pred. No. 19; Mismatches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
Qy 3 DPOETYGALDGGSQ 19
Db 211 DPLKTTGIVELGGASQ 227

Search completed: February 11, 2003, 18:40:02
 Job time : 18 secs

GenCore version 5.1.3
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Om protein - protein search, using sw model

Run on: February 11, 2003, 18:22:16 ; Search time 11 seconds
(without alignments) 71.641 Million cell updates/sec

Title: US-09-781-796b-7

perfect score: 96
Sequence: 1 KSDMGETYKALDGGASQ 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40; *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	92	95.8	510	1 ENPL_PIG	09myu4 sus scrofa
2	92	95.8	513	1 ENPL_BOVIN	01895 bos taurus
3	78.5	510	1 ENPL_HUMAN	P4961 homo sapien	
4	75	78.1	510	1 ENPL_MOUSE	P55772 mus musculus
5	66	68.8	511	1 ENPL_RAT	P97687 rattus norvegicus
6	65	67.7	469	1 ENPL_MEASU	09qpc8 mesocricetus auratus
7	64	66.7	427	1 ENPL_MOUSE	09wuzz mus musculus
8	64	66.7	428	1 ENPL_HUMAN	075356 homo sapiens
9	64	66.7	529	1 ENPL_HUMAN	075355 homo sapien
10	58	60.4	493	1 ENPL_CHICK	093395 gallus gallus
11	56	58.3	495	1 ENPL_HUMAN	09513 homo sapien
12	56	58.3	495	1 ENPL_MOUSE	055026 mus musculus
13	56	58.3	495	1 ENPL_RAT	035795 rattus norvegicus
14	54	494	1 ENPL_CHICK	P79784 gallus gallus	
15	52	54.2	630	1 YNL1_YEAST	P40099 saccharomyces cerevisiae
16	50	52.1	552	1 YE04_CAEEL	021815 caenorhabditis elegans
17	48	50.0	453	1 YNL1_RAT	09er31 rattus norvegicus
18	48	50.0	613	1 ENPL_MOUSE	09drb4 mus musculus
19	47	49.0	124	1 PRO2_DICTI	P26200 dictyostelia dictyostelia
20	47	49.0	616	1 ENPL_HUMAN	09Y227 homo sapiens
21	46	47.9	484	1 ENPL_HUMAN	075354 homo sapien
22	44	45.8	204	1 RX3_GUTH	046894 gilliardia
23	44	45.8	253	1 YNL1_MYCTU	011026 mycobacterium
24	45.8	372	1 YNC_ECOLI	P39353 escherichia coli	
25	44	45.8	455	1 NTPA_PEA	P52914 pistium sativum
26	41	42.7	454	1 APY_SOJU	P80595 solanum tuberosum
27	41	42.7	519	1 ZN35_HUMAN	P13682 homo sapiens
28	40	41.7	439	1 PRS4_DROME	P4601 drosophila melanogaster
29	40	41.7	485	1 YYE_CAEEL	018411 caenorhabditis elegans
30	40	41.7	808	1 YNE_ECOLI	P77374 escherichia coli
31	40	41.7	818	1 SNF3_YEAST	P10870 saccharomyces cerevisiae
32	39	40.6	294	1 MIAA_STRPN	09chu2 lactococcus
33	39	40.6	1	MIAA_STRPN	097rw5 streptococcus

ALIGNMENTS

RESULT 1	ID	ENPL_PIG	STANDARD;	PRM:	510 AA.
AC	Q9mt04;				
DT	16-OCT-2001	(Rel. 40, created)			
DT	16-OCT-2001	(Rel. 40, last sequence update)			
DT	16-OCT-2001	(Rel. 40, last annotation update)			
DE	(NPase1)	Ecto-ATP triphosphatase (NPase1) (ATPase) (Lymphoid cell activation antigen) (Ecto-aprase) (CD39 antigen).			
DE	ENTPD1	ENTPD1 OR CD39.			
OS	Sus scrofa (pig)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Etherida; Cetartiodactyla; Suina; Suidae; Sus.				
OX					
RN	[1]				
RP					
RC					
RA	Lemmens R., Vanduffel L., Kittel A., Beaudoin A.R., Benrezzak O., Sevigny J.;				
RT	"Distribution, cloning, and characterization of porcine nucleoside triphosphate diiphosphohydrolase-1";				
RL	Bur. J. Biochem. 267:4106-4114(2000).				
RN	[12]				
RP	SEQUENCE OF 202-220.				
RC	TISSUE="Pancreas"; MEDLINE=97113858; PubMed=995160;				
RX	Kaczmarek E., Kozlak K., Sevigny J., Siegel J.B., Anrather J., Beaudoin A.R., Bach F.H., Robson S.C.; Debeauvoir A.R., Bach F.H., Robson S.C.; RT "Identification and characterization of CD39/vascular ATP diiphosphohydrolase";				
RL	J. Biol. Chem. 271:33116-33122(1996);				
CC	-- FUNCTION: IN THE NERVOUS SYSTEM, COULD HYDROLYSE ATP AND OTHER NUCLEOTIDES TO REGULATE POKINERGIC NEUROTRANSMISSION. COULD ALSO BE IMPLICATED IN THE PREVENTION OF PLATELET AGGREGATION.				
CC	-- HYPOTHESIS: COULD HYDROLYZE ATP AND ADP EQUALLY WELL.				
CC	-- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.				
CC	-- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM (BY SIMILARITY).				
CC	-- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).				
CC	-- SUBCELLULAR LOCATION: Integral membrane protein (Potential).				
CC	-- TISSUE SPECIFICITY: HIGHEST EXPRESSION FOUND IN VASCULAR ENDOTHELIUM, SMOOTH MUSCLE, SPLEEN AND LUNG.				
CC	-- PTM: CLEAVED IN TWO POLYPEPTIDES THAT SEEM TO STAY TOGETHER BY NONCOVALENT INTERACTIONS.				
CC	-- SIMILARITY: BELONGS TO THE CD39/NPase FAMILY.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
DR	EMBL: AJ13746; CAB95871.1; -				

[3] SEQUENCE FROM N.A. (ISOFORMS PLACENTAL I AND II).
 RN RP PF001150; GDAL_CD39; 1.
 RC TISSUE=placenta;
 RX MEDLINE=99332082; PubMed=10405171;
 RA Matsumoto M., Sakurai Y., Kokubo T., Yagi H., Makita K., Matsui T.,
 RA Titani K., Fujimura Y., Narita N.;
 RT i-The cDNA cloning of human placental ecto-ATP diphosphohydrolases I
 RT and II.;"
 RL FEBS Lett. 453:335-340(1999).
 RN [4] SEQUENCE OF 240-242; 162-166; 185-189; 210-223; 243-249 AND 288-297.
 RC TISSUE=placenta;
 RX MEDLINE=96096723; PubMed=9529670;
 RA Christoforidis S., Pamarcaki T., Galaris D., Kellner R., Tsolias O.,
 RA Eur. J. Biochem. 234:66-74(1995).
 RN SEQUENCE OF 1-30; 49-65; 94-97; 88-93; 193-223; 245-265; 382-385 AND
 RP 399-405 (ISOFORM PLACENTAL I).
 RC TISSUE=placenta;
 RX MEDLINE=99062444; PubMed=9846014;
 RA Makita K., Shimojima T., Sakurai Y., Yagi H., Matsumoto M., Narita N.,
 RA Sakamoto Y., Saito S., Ikeda Y., Suzuki M., Titani K., Fujimura Y.;
 RT "Placental ecto-ATP diphosphohydrolase: its structural feature
 RT distinct from CD39, localization and inhibition on shear-induced
 RT platelet aggregation.";
 RL Int. J. Hematol. 68:297-310(1998).
 RN [6] FUNCTION.
 RX MEDLINE=97115888; PubMed=8955160;
 RA Kazmarek F., Kozlak K., Sevigny J.J., Siegel J.B., Anrather J.,
 RA Beaudoin A.R., Bach F.H., Robson S.C.;
 RT "Identification and characterization of CD39/vascular ATP
 RT diphosphohydrolase";
 RL J. Biol. Chem. 271:33116-33122(1996).
 CC -!- FUNCTION: IN THE NERVOUS SYSTEM, COULD HYDROLYSE ATP AND OTHER
 CC NUCLEOTIDES TO REGULATE PURINERGIC NEUROTRANSMISSION. COULD ALSO
 BE IMPLICATED IN THE PREVENTION OF PLATELET AGGREGATION.
 CC HYDROLYSES ATP AND ADP EQUALLY WELL.
 CC -!- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
 CC -!- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.
 CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (potential).
 CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS: VASCULAR (SHOWN HERE), PLACENTAL
 CC I AND PLACENTAL II; ARE PRODUCED BY ALTERNATIVE SPlicing.
 CC -!- TISSUE SPECIFICITY: EXPRESSED PRIMARILY ON ACTIVATED LYMPHOID
 CC CELLS. ALSO EXPRESSED IN ENDOTHELIAL TISSUES. THE VASCULAR ISOFORM
 CC AND THE PLACENTAL ISOFORM I ARE PRESENT IN BOTH PLACENTA AND
 CC UMBILICAL VEIN, WHEREAS PLACENTAL ISOFORM I IS PRESENT IN PLACENTA
 CC ONLY.
 CC -!- PTM: THE N-TERMINUS IS BLOCKED.
 CC -!- MISCELLANEOUS: OPTIMAL PH IS 7.0-7.5 WITH ATP AS SUBSTRATE AND
 CC 7.5-8.0 WITH ADP.
 CC -!- SIMILARITY: BELONGS TO THE GDAL / CD39 NTPASE FAMILY.
 CC -!- DATABASE: NAME=PROK; NOTE=CD guide CD39 entry;
 CC WWW=<http://www.ncbi.nlm.nih.gov/prok/ed/cd39.htm>".

RESULT 4

ID	ENPL_MOUSE	STANDARD:	PRT:	510 AA.
AC	P55772;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01 NOV-1997 (Rel. 35, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5) (Ntpbase) (Ecto-ATP diphosphohydrolase) (Ntpbase) (Lymphoid cell activation antigen) (Ecto-apyrase) (CD39 antigen).			
DE	DEPTDI OR CD39.			
GN				
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TAXID=10090;			
OX				
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95015846; PubMed=7930580;			
RA	Maliszewski C.R., Delespesse G.J.T., schoenborn M.A., Armitage R.J., RA Fanslow W.C., Nakajima T., Baker E., Sutherland G.R., Poindexter K., RA Birks C., Alpern A., Friend D., Gimbel S.D., Gayle R.B. III; RT "The CD39 lymphoid cell activation antigen. Molecular cloning and RT structural characterization."; J. Immunol. 153:3574-3583(1994). RA [2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=129/SVJ;			
RX	MEDLINE=9839981; PubMed=970622;			
RA	Schoenborn M.A., Jenkins N.A., Copeland N.G., Gilbert D.J., Gayle R.B. III, Maliszewski C.R.;			
RT	"Gene structure and chromosome location of mouse Cd39 coding for an RT ecto-apyrase.";			
RL	Cytogenet. Cell Genet. 81:287-299(1998).			
CC	-!- FUNCTION: IN THE NERVOUS SYSTEM, COULD HYDROLYSE ATP AND OTHER CC NUCLEOTIDES TO REGULATE PURINERGIC NEUROTRANSMISSION. COULD ALSO CC BE IMPLICATED IN THE PREVENTION OF PLATELET AGGREGATION.			
CC	HYDROLYZES ATP AND ADP EQUALLY WELL.			

DR PIAM; PF001150; GDAL_CD39; 1.
 DR PROSITE; PS01238; GDAL_CD39_NT_PASE; 1.
 KW Hydrolase; Transmembrane; Antigen; Glycoprotein; Calcium; Magnesium;
 KW Alternative splicing; CYTOPLASMIC (POTENTIAL).
 KW DOMAIN 1 16 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 17 37 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 38 478 POTENTIAL.
 FT TRANSMEM 479 499 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 500 510 CYTOPLASMIC (POTENTIAL).
 FT CARBOHD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 227 227 N LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 371 371 N LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 1 4 MEDT-> MKTKTDTSQ (IN ISOFORM PLACENTAL I AND ISOFORM PLACENTAL II).
 FT VARSPLIC 272 299 V-> Y (IN REF. 5).
 FT VARSPLIC 300 510 MISSING (IN ISOFORM PLACENTAL II).
 FT VARSPLIC 57 58 SS -> G (IN REF. 5).
 FT CONFLICT 162 D -> K (IN REF. 4).
 FT CONFLICT 208 T -> TGET (IN REF. 5).
 FT CONFLICT 248 V -> Y (IN REF. 5).
 FT SEQUENCE 5 10 AA: 57964 MW: BAD87D24595649159 CRC64:
 SQ

Oy 1 KSDPQETGALDDGGSTQ 19
 Query Match 78.1%; Score 75; DB 1; Length 510;
 Best Local Similarity 73.7%; Pred. No. 2.3e-05;
 Matches 14; Conservative 4; Mismatches 1; Indels 0; gaps 0;

Db 202 ETNNQETFGALDDGGSTQ 220

DE Ectonucleoside triphosphate diphosphohydrolase 5 precursor (EC 3.6.1.6) (NTPdase5) (Nucleoside diphosphatase) (CD39 antigen-like DE 4) (ER-UDPase) (proto-oncogene cph).

GN ENTPD5 OR CD39L4 OR CPH.

OS Mesocricetus auratus (Golden hamster).

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; Mesoicetus.

OC NCBI_TaxID=1036;

RN [1]

RX SEQUENCE FROM N.A. PubMed=9988819;

RX MEDLINE=91147925; PubMed=9457681;

RT "The product of the cph oncogene is a truncated, nucleotide-binding protein that enhances cellular survival to stress.";

RL Oncogene 18:689-701(1999).

CC FUNCTION: LIKELY TO PROMOTE REGLYCOSYLATION REACTIONS INVOLVED IN GLYCOPROTEINS FOLDING AND QUALITY CONTROL IN THE ENDOPLASMIC RETICULUM. HYDROLYSES UDP, GDP AND IDP BUT NOT ANY OTHER NUCLEOSIDE DI-, MONO- OR TRIPHOSPHATES NOR THIAMINE PYROPHOSPHATE (BY SIMILARITY).

CC CATALYTIC ACTIVITY: A nucleoside diphosphate + H₂O = a nucleotide + phosphate.

CC -I COFACTOR: REQUIRES CALCIUM AND MAGNESTIUM (BY SIMILARITY).

CC -I SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).

CC -I TISSUE SPECIFICITY: EXPRESSED IN FETAL CELLS AND MOST ADULT TISSUES.

CC -I DISEASE: CPH ONCOGENE HAS TRANSFORMING CAPACITY AND TUMORIGENIC POTENTIAL.

CC -I SIMILARITY: BELONGS TO THE GDAL / CD39 NTPASE FAMILY.

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CC EMBL: AF084568; AAP22931.1; ALT_TERM.

CC EMBL: AF084569; AAF22932.1; -; GDAL_CD39_NTPase.

DR InterPro: IPR000407; GDAL_CD39; 1.

DR Pfam: PF01150; GDAL_CD39; 1.

DR PROSITE: PS01238; GDAL_CD39_NTPASE; FALSE NEG.

KW Hydrolase; Transmembrane; Glycoprotein; Calcium; Magnesium; Endoplasmic reticulum; Signal; proto-oncogene.

FT SIGNAL 1 18 POTENTIAL.

FT CHAIN 19 469

FT CARBOHYD 42 42 N-LINKED (GLCNAC- . .) (POTENTIAL).

FT CARBOHYD 232 232 N-LINKED (GLCNAC- . .) (POTENTIAL).

SQ 469 AA: 52125 MW: 03D8A23E0C73474B CRC64;

RESULT 7

ENSP_MOUSE STANDARD; PRT; 427 AA.

AC O9WU29; O70214; -

DT 16-OCT-2001 (rel. 40, 'Created')

DT 16-OCT-2001 (rel. 40, 'Last sequence update')

DT 16-OCT-2001 (rel. 40, 'Last annotation update')

DE Ectonucleoside triphosphate diphosphohydrolase 5 precursor (EC 3.6.1.6) (NTPdase5) (Nucleoside diphosphatase) (CD39 antigen-like DE 4) (ER-UDPase).

GN ENTPD5 OR CD39L4.

MUS musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; Mesoicetus.

OC NCBI_TaxID=10090;

RN [1]

RX SEQUENCE FROM N.A.

RX MEDLINE=98119025; PubMed=9457681;

RT "cDNA cloning and chromosomal mapping of a mouse gene with homology to NPases.";

RA Chadwick B.P., Williamson J., Sheer D., Frischauft A.-M.; Mamm. Genome 9:162-164 (1998).

RC TISSUE=Liver;

RX MEDLINE=99298181; PubMed=10369669;

RT Trombetta, E.S., Heinenius A.;

RT Glycoprotein reglycosylation and nucleotide sugar utilization in the secretory pathway: identification of a nucleoside diphosphatase in the endoplasmic reticulum.;

RT Embro J. 18:3282-3292(1999).

RN [3]

RX SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Kidney;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto T., Aizawa K., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Battalov S., Cassavant T., Fleischmann W., Gaasterland T., Glissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido T., Pesole G., Quackenbush J., Schriml L.M., Straub F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Ohido T., Furuno M., Aono H., Baldarelli R., Barsh G., Suzuki H., Toyokawa K., Wang K.H., Weltz C., Whittaker C., de Bonaloo M.F., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaloo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hoffman M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombretti P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Suya T., Shibaoka T., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilmung L., Wynnshaw-Boriss A., Yoshida K., Hasagawa Y., Kawaji H., Kohitsuki S., RA Hayashihashi Y.;

RA "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:645-650(2001).

CC -I FUNCTION: LIKELY TO PROMOTE REGLYCOSYLATION REACTIONS INVOLVED IN GLYCOPROTEINS FOLDING AND QUALITY CONTROL IN THE ENDOPLASMIC RETICULUM. HYDROLYSES UDP, GDP AND IDP BUT NOT ANY OTHER NUCLEOSIDE DI-, MONO- OR TRIPHOSPHATES, NOR THIAMINE PYROPHOSPHATE.

CC -I CATALYTIC ACTIVITY: A nucleoside diphosphate + H₂O = a nucleotide + phosphate.

CC -I COFACTOR: REQUIRES CALCIUM AND MAGNESTIUM.

CC -I SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.

CC -I TISSUE SPECIFICITY: UNIQUOTOUS.

CC -I PTM: GLYCOSYLATED WITH HIGH MANNOSE N-LINKED GLYCANS.

CC -I MISCELLANEOUS: OPTIMAL PH IS NEUTRAL.

CC -I SIMILARITY: BELONGS TO THE GDAL / CD39 NTPASE FAMILY.

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CC EMBL: AF006482; AAC05181.1; -

DR EMBL: AJ236636; CABAB533.1; -

DR EMBL: AK002618; BAB2224.1; -

DR MGDB: MGJ:121138; Entpd5

DR InterPro: IPR000407; GDAL_CD39_NTPase.

DR Pfam: PF01150; GDAL_CD39; 1.

DR	PROSTATE; PS01238; GDAL_CD39_NTPOSE; FALSE_NEG.
KW	Hydrolase; Transmembrane; Glycoprotein; Calcium; Magnesium;
KW	Endoplasmic reticulum; Glycoprotein; Calcium; Magnesium;
FT	SIGNAL
FT	CHAIN
FT	19 427
FT	POTENTIAL.
FT	ECTONUCLEOSIDE TRIPHOSPHATE
FT	DIPHOSP-HYDROLYASE 5.
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	F -> L (IN REF. 1).
FT	DGTLQLKVKVNTIGVALGATPHILQSLGITS -> ERH
FT	PLTARKRSEQRHDLIGLGHUSPAPVSGHOLRSSTSPAC
FT	ISPEVFSQGSDTSFESDLSKAMPER (IN REF. 1).
SQ	SEQUENCE 427 AA; 47101 MW; 289DA2C342C5557 CRC64;
Qy	5 QEYGA(DLG)GASTQ 19
Db	191 QEVGT(LDG)GASTQ 205
RESULT 8	
ID	ENP5_HUMAN
AC	075356;
DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DE	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Retonucleoside triphosphate diiphosphohydrolase 5 precursor,
(EC 3.6.1.6) (NTPDase5) (Nucleoside diiphosphatase) (CD39 antigen-like	
DE	4) (ER-UDPase).
DE	ENTPD5 OR CD39A.
OS	Hom sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;
OC	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Leukemia;
RX	MEDLINE=98341119; PubMed=9676430;
RA	Chadwick B.P., Frischknecht A.-M.;
RT	"The CD39-like gene family"; identification of three new human members (CD39a, CD39b, and CD39c), their murine homologues, and a member of the gene family from Drosophila melanogaster.";
RT	Genomics 50:557-567(1998).
-!- FUNCTION: LIKELY TO PROMOTE REGULOCYTOLYSIS REACTIONS INVOLVED IN GLYCOPROTEINS FOLDING AND QUALITY CONTROL IN THE ENDOPASMIC RETICULUM. HYDROLYSES UDP, GDP AND IDP BUT NOT ANY OTHER NUCLEOSIDE DI-, MONO- OR TRIPHOSPHATES, NOR THIAMINE PROPHOSPHATE (BY SIMILARITY).	
-!- CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)O = a nucleotide + phosphate.	
-!- COFACTOR: REQUIRES CALCIUM AND MAGNESTUM.	
-!- TISSUE SPECIFICITY: EXPRESSED IN ADULT LIVER, KIDNEY, PROSTATE, TESTIS AND COLON. MUCH WEAKER EXPRESSION IN OTHER TISSUES.	
-!- SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPOSE FAMILY.	
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EMBL; AF039918; AAC39885; 1; .	
Gene: HGNC:3367; ENTPD5.	
MM: 603162;	
InterPro: IPR000407; GDA1_CD39_NTPase.	
Prtn: PF01150; GDAL_CD39; 1.	
RESULT 9	
ID	ENP3_HUMAN
AC	075355; 060495;
DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DE	16-OCT-2001 (Rel. 40, Last annotation update)
DE	(NTPDase3) (Ecto-ATP diphosphohydrolase) (ATPase)
DE	(CD39 antigen-like 3) (HB6).
GN	ENTPD3 OR CD39L3.
OS	Hom sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Keratinocytes;
RX	MEDLINE=98341119; PubMed=9676430;
RA	Chadwick B.P., Frischknecht A.-M.;
RT	"The CD39-like gene family"; identification of three new human members (CD39a, CD39b, and CD39c), their murine homologues, and a member of the gene family from Drosophila melanogaster.";
RT	Genomics 50:557-567(1998).
RN	[2]
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC	TISSUE=brain;
RX	MEDLINE=98341144; PubMed=967246;
RA	Smith T.M., Kirby T.L.;
RT	"Cloning, sequencing, and expression of a human brain ecto-apyrases related to both the ecto-ATPases and CD39 ecto-apyrases.";
RT	Biochim. Biophys. Acta 1386:65-78(1998).
RN	[3]
RP	REVISIONS.
RA	Smith T.M., Kirby T.L.;
RA	Submitted (APR 2001) to the EMBL/GenBank/DDBJ databases.
RN	[4]
RP	MUTAGENESIS OF TRP-187; ASP-219 AND TRP-459.
RX	MEDLINE=9924975; PubMed=10331556;
RA	Smith T.M., Lewis Carl S.A., Kirby T.L.;
RT	"Mutagenesis of two conserved tryptophan residues of the E-type ATPases: inactivation and conversion of an ecto-apyrase to an ecto-NPase.";
RT	Biochemistry 38:5849-5857(1999).
RN	[5]
RP	MUTAGENESIS OF R-67, R-143; R-146; E-182; N-191; S-224 AND Q-226.
RX	MEDLINE=21197753; PubMed=11300774;
RA	Yang F., Hicks-Bergen C.A., Smith T.M., Kirby T.L.;
RT	"Site-directed mutagenesis of human nucleoside triphosphate diphosphohydrolase 3: the importance of residues in the apyrase conserving regions";
RT	Biochemistry 10:3943-3950(2001).
RN	[6]

CC	OVER ADP.	DE	Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
CC	- CATALYTIC ACTIVITY: ATP + 2 H ₂ O = AMP + 2 phosphate.	DE	(NTPase) (Ecto-ATP diphosphohydrolase) (ATPase) (Lymphoid
CC	- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.	DE	activation antigen) (Ecto-apyrase) (CD39 antigen).
CC	- SUBCELLULAR LOCATION: Integral membrane protein (Potential).	GN	ENTPD1 OR CD39.
CC	- TISSUE SPECIFICITY: EXPRESSED IN ADULT BRAIN, PANCREAS, SPLEEN AND PROSTATE. MODERATE OR LOW EXPRESSION IS SEEN IN MOST TISSUES. NOT EXPRESSED IN LIVER AND PERIPHERAL BLOOD LEUKOCYTES.	OS	Gallus gallus (chicken)
CC	- SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.	OC	Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus Gallus
DR	EMBL: AF039917; AAC39884.1; -.	OX	NCBITaxID=9031;
DR	GenBank: HGNC-3365; ENPPD3.	RN	[1] Nucleotide sequence of the chicken oviduct ecto-ATPase. Lewis-Carl S., Kirley T.L.; RT
DR	MIM: 603161; -.	RA	"Immunolocalization of the ecto-ATPase and ecto-apyrase in chicken gizzard and stomach. Purification and N-terminal sequence of the stomach ecto-apyrase".
DR	InterPro: IPR000407; GDA1_CD39_NTPase.	RT	J. Biol. Chem. 272:23645-23652(1997).
DR	Pfam: PF0150; GDA1_CD39; 1.	RL	- FUNCTION: IN THE NERVOUS SYSTEM, COULD HYDROLYSE ATP AND OTHER NUCLEOTIDES TO REGULATE PURINERGIC NEUROTRANSMISSION. COULD ALSO BE IMPLICATED IN THE PREVENTION OF PLATELET AGGREGATION.
FT	TRANSEM	CC	HYDROLYSES ATP AND ADP EQUALLY WELL (BY SIMILARITY).
FT	DOMAIN	CC	- CATALYTIC ACTIVITY: ATP + 2 H ₂ O = AMP + 2 phosphate.
FT	CARBOHYD	CC	- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM (BY SIMILARITY).
FT	CARBONYD	CC	- SUBUNIT: HOMODIMER DISULFIDE-LINKED (PROBABLE).
FT	CARBOHYD	CC	- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
FT	CARBOHYD	CC	- PTM: N-GLYCOSYLATED.
FT	CARBONYD	CC	- SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
FT	CARBONYD	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
FT	MUTAGEN	CC	->G: INCREASE OF ACTIVITY.
FT	MUTAGEN	CC	R->A: LOSS OF ACTIVITY.
FT	MUTAGEN	CC	R->K: INCREASE OF ACTIVITY.
FT	MUTAGEN	CC	R->N: NO EFFECT.
FT	MUTAGEN	CC	R->P: INCREASE OF ATPase ACTIVITY,
FT	MUTAGEN	CC	DECREASE OF ATPase ACTIVITY.
FT	MUTAGEN	CC	R->T: INCREASE OF ACTIVITY.
FT	MUTAGEN	CC	R->D: COMPLETE LOSS OF ACTIVITY.
FT	MUTAGEN	CC	R->Q: COMPLETE LOSS OF ACTIVITY.
FT	MUTAGEN	CC	N->A: COMPLETE LOSS OF ACTIVITY.
FT	MUTAGEN	CC	W->A: INCREASE OF ACTIVITY, INCREASE OF ATP HYDROLYSIS.
FT	MUTAGEN	CC	V->A (IN REF. 3).
FT	CONFLICT	CC	D->E: INCREASE OF ACTIVITY.
FT	SEQUENCE	CC	S->A: COMPLETE LOSS OF ACTIVITY.
Query Match	64.6%; Score 62; DB 1; Length 529;	DR	EMBL: AF041355; AAC26491.1; -.
Best Local Similarity	92.9%; Pred. No. 0.0045; 1;	DR	InterPro: IPR000407; GDA1_CD39_NTPase.
Matches	13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	DR	Pfam: PF0150; GDA1_CD39; 1.
Oy	6 ETYGALDGGASTQ 19	DR	PROSITE: PS01238; GDA1_CD39_NTPase; 1.
Db	213 ETYGALDGGASTQ 226	DR	Hydrolase; Transmembrane; Antigen; Glycoprotein; Calcium; Magnesium.
RESULT 10		FT	Hydrolase; Transmembrane; Antigen; Glycoprotein; Calcium; Magnesium.
ID	ENPL_CHICK	FT	Hydrolase; Transmembrane; Antigen; Glycoprotein; Calcium; Magnesium.
AC	ENPL_CHICK STANDARD; PRT: 493 AA.	FT	Hydrolase; Transmembrane; Antigen; Glycoprotein; Calcium; Magnesium.
09395;		FT	Hydrolase; Transmembrane; Antigen; Glycoprotein; Calcium; Magnesium.
DT	16-OCT-2001 (Rel. 40, Created)	FT	Hydrolase; Transmembrane; Antigen; Glycoprotein; Calcium; Magnesium.
DT	16-OCT-2001 (Rel. 40, Last sequence update)	FT	Hydrolase; Transmembrane; Antigen; Glycoprotein; Calcium; Magnesium.
DT	16-OCT-2001 (Rel. 40, Last annotation update)	FT	Hydrolase; Transmembrane; Antigen; Glycoprotein; Calcium; Magnesium.

Matches	12;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;	FT	CARBHYD	64	64	N-LINKE	(GLCNAC. . .)	(POTENTIAL).	
QY	6	ETYGALDGCASTQ	19							FT	CARBHYD	129	129	N-LINKE	(GLCNAC. . .)	(POTENTIAL).	
ID	ENP2_HUMAN	STANDARD;		PRT;	495 AA.					FT	CARBHYD	294	294	N-LINKE	(GLCNAC. . .)	(POTENTIAL).	
RP	09Y5LJ; 015464;									FT	CARBHYD	378	378	N-LINKE	(GLCNAC. . .)	(POTENTIAL).	
DT	16-OCT-2001	(Rel. 40; Created)								FT	CARBHYD	443	443	N-LINKE	(GLCNAC. . .)	(POTENTIAL).	
DT	16-OCT-2001	(Rel. 40; Last sequence update)								FT	VARSPLIC	383	405	MISSING (IN SHORT ISOFORM).			
DE	Ectonucleoside triphosphate diphosphohydrolase 2 (EC 3.6.1.3)									SQ	SEQUENCE	495 AA;	53665 MW;	3BDBA14A679B422 CRG64;			
DE	(NTPase2) (Ecto-ATPase) (CD39 antigen-like 1).									Query	Match	58.3%	Score 56;	DB 1;	Length 495;		
GN	ENPBP2 OR CD39L.									Best Local Similarity	84.6%	Pred. No. 0.046;					
OS	Homo sapiens (Human).									Matches	11;	Conservative	1;	Mismatches	1;	Indels	0;
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OX									Db	196	TLGAMDLLGGASTQ	208				
RA	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.									RESULT	12						
RA	NCBI_TAXID=9606;									Query	Match	58.3%	Score 56;	DB 1;	Length 495;		
RN	[1]									Best Local Similarity	84.6%	Pred. No. 0.046;					
RP	SEQUENCE FROM N.A. (SHORT FORM).									Matches	11;	Conservative	1;	Mismatches	1;	Indels	0;
RC	TISSUE=Keratinocytes;									Db	196	TLGAMDLLGGASTQ	208				
RY	MEDLINE=97419269; PubMed=9271669;									QY	7	TYGALDLGGASTQ	19				
RA	Chadwick B.P., Frischau A.-M.;									Query	Match	58.3%	Score 56;	DB 1;	Length 495;		
RA	"Cloning and mapping of a human and mouse gene with homology to ecto-ATPase genes"; [2]									Best Local Similarity	84.6%	Pred. No. 0.046;					
RA	RT									Matches	11;	Conservative	1;	Mismatches	1;	Indels	0;
RA	RT									Db	196	TLGAMDLLGGASTQ	208				
RA	RT									RESULT	12						
RA	RT									Query	Match	58.3%	Score 56;	DB 1;	Length 495;		
RA	RT									Best Local Similarity	84.6%	Pred. No. 0.046;					
RA	RT									Matches	11;	Conservative	1;	Mismatches	1;	Indels	0;
RA	RT									Db	196	TLGAMDLLGGASTQ	208				
RA	RT									QY	7	TYGALDLGGASTQ	19				
RA	RT									Query	Match	58.3%	Score 56;	DB 1;	Length 495;		
RA	RT									Best Local Similarity	84.6%	Pred. No. 0.046;					
RA	RT									Matches	11;	Conservative	1;	Mismatches	1;	Indels	0;
RA	RT									Db	196	TLGAMDLLGGASTQ	208				
RA	RT									QY	7	TYGALDLGGASTQ	19				
RA	RT									Query	Match	58.3%	Score 56;	DB 1;	Length 495;		
RA	RT									Best Local Similarity	84.6%	Pred. No. 0.046;					
RA	RT									Matches	11;	Conservative	1;	Mismatches	1;	Indels	0;
RA	RT									Db	196	TLGAMDLLGGASTQ	208				
RA	RT									QY	7	TYGALDLGGASTQ	19				
RA	RT									Query	Match	58.3%	Score 56;	DB 1;	Length 495;		
RA	RT									Best Local Similarity	84.6%	Pred. No. 0.046;					
RA	RT									Matches	11;	Conservative	1;	Mismatches	1;	Indels	0;
RA	RT									Db	196	TLGAMDLLGGASTQ	208				
RA	RT									QY	7	TYGALDLGGASTQ	19				
RA	RT									Query	Match	58.3%	Score 56;	DB 1;	Length 495;		
RA	RT									Best Local Similarity	84.6%	Pred. No. 0.046;					
RA	RT									Matches	11;	Conservative	1;	Mismatches	1;	Indels	0;
RA	RT									Db	196	TLGAMDLLGGASTQ	208				
RA	RT									QY	7	TYGALDLGGASTQ	19				
RA	RT									Query	Match	58.3%	Score 56;	DB 1;	Length 495;		
RA	RT									Best Local Similarity	84.6%	Pred. No. 0.046;					
RA	RT									Matches	11;	Conservative	1;	Mismatches	1;	Indels	0;
RA	RT									Db	196	TLGAMDLLGGASTQ	208				
RA	RT									QY	7	TYGALDLGGASTQ	19				
RA	RT									Query	Match	58.3%	Score 56;	DB 1;	Length 495;		
RA	RT									Best Local Similarity	84.6%	Pred. No. 0.046;					
RA	RT									Matches	11;	Conservative	1;	Mismatches	1;	Indels	0;
RA	RT									Db	196	TLGAMDLLGGASTQ	208				
RA	RT									QY	7	TYGALDLGGASTQ	19				
RA	RT									Query	Match	58.3%	Score 56;	DB 1;	Length 495;		
RA	RT									Best Local Similarity	84.6%	Pred. No. 0.046;					
RA	RT									Matches	11;	Conservative	1;	Mismatches	1;	Indels	0;
RA	RT									Db	196	TLGAMDLLGGASTQ	208				
RA	RT									QY	7	TYGALDLGGASTQ	19				
RA	RT									Query	Match	58.3%	Score 56;	DB 1;	Length 495;		
RA	RT									Best Local Similarity	84.6%	Pred. No. 0.046;					
RA	RT									Matches	11;	Conservative	1;	Mismatches	1;	Indels	0;
RA	RT									Db	196	TLGAMDLLGGASTQ	208				
RA	RT									QY	7	TYGALDLGGASTQ	19				
RA	RT									Query	Match	58.3%	Score 56;	DB 1;	Length 495;		
RA	RT									Best Local Similarity	84.6%	Pred. No. 0.046;					
RA	RT									Matches	11;	Conservative	1;	Mismatches	1;	Indels	0;
RA	RT									Db	196	TLGAMDLLGGASTQ	208				
RA	RT									QY	7	TYGALDLGGASTQ	19				
RA	RT									Query	Match	58.3%	Score 56;	DB 1;	Length 495;		
RA	RT									Best Local Similarity	84.6%	Pred. No. 0.046;					
RA	RT									Matches	11;	Conservative	1;	Mismatches	1;	Indels	0;
RA	RT									Db	196	TLGAMDLLGGASTQ	208				
RA	RT									QY	7	TYGALDLGGASTQ	19				
RA	RT									Query	Match	58.3%	Score 56;	DB 1;	Length 495;		
RA	RT									Best Local Similarity	84.6%	Pred. No. 0.046;					
RA	RT									Matches	11;	Conservative	1;	Mismatches	1;	Indels	0;
RA	RT									Db	196	TLGAMDLLGGASTQ	208				
RA	RT									QY	7	TYGALDLGGASTQ	19				
RA	RT									Query	Match	58.3%	Score 56;	DB 1;	Length 495;		
RA	RT									Best Local Similarity	84.6%	Pred. No. 0.046;					
RA	RT									Matches	11;	Conservative	1;	Mismatches	1;	Indels	0;
RA	RT									Db	196	TLGAMDLLGGASTQ	208				
RA	RT									QY	7	TYGALDLGGASTQ	19				
RA	RT									Query	Match	58.3%	Score 56;	DB 1;	Length 495;		
RA	RT									Best Local Similarity	84.6%	Pred. No. 0.046;					
RA	RT									Matches	11;	Conservative	1;	Mismatches	1;	Indels	0;
RA	RT									Db	196	TLGAMDLLGGASTQ	208				
RA	RT									QY	7	TYGALDLGGASTQ	19				
RA	RT									Query	Match	58.3%	Score 56;	DB 1;	Length 495;		
RA	RT									Best Local Similarity	84.6%	Pred. No. 0.046;					
RA	RT									Matches	11;	Conservative	1;	Mismatches	1;	Indels	0;
RA	RT									Db	196	TLGAMDLLGGASTQ	208				
RA	RT									QY	7	TYGALDLGGASTQ	19				
RA	RT									Query	Match	58.3%	Score 56;	DB 1;	Length 495;		
RA	RT									Best Local Similarity	84.6%	Pred. No. 0.046;					
RA	RT									Matches	11;	Conservative	1;	Mismatches	1;	Indels	0;
RA	RT									Db	196	TLGAMDLLGGASTQ	208				
RA	RT									QY	7	TYGALDLGGASTQ	19				
RA	RT									Query	Match	58.3%	Score 56;	DB 1;	Length 495;		
RA	RT									Best Local Similarity	84.6%	Pred. No. 0.046;					
RA	RT									Matches	11;	Conservative	1;	Mismatches	1;	Indels	0;
RA	RT									Db							

CC	ADP ONLY TO A MARGINAL EXTENT (BY SIMILARITY).	RT	"An ecto-ATPase and an ecto-ATP diphosphohydrolase are expressed in rat brain.";
CC	-!- CATALYTIC ACTIVITY: ATP + H ₂ O = ADP + phosphate.	RT	Neuropharmacology 36:1189-1200(1997).
CC	-!- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.	RL	[2]
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).	RN	SEQUENCE FROM N.A. (ISOFORM 1).
CC	-! ALTERNATIVE PRODUCTS: Isoforms; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.	RP	STRAIN=Wistar; TISSUE=Cochlea;
CC	-!- INDUCTION: BY DIOXIN.	RC	MEDLINE=2112474; PubMed=11229804;
CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.	RX	Lu Q., Porter L.D., Cui X., Sanborn B.M.;
CC	-!- SIMILARITY: BELONGS TO THE GDAL / CD39 NTPASE FAMILY.	RA	"Ecto-ATPase mRNA is regulated by FSH in Sertoli cells.";
CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.	RL	J. Androl. 22:289-301(2001).
CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.	RN	[3]
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	RP	SEQUENCE OF 379-495 FROM N.A. (ISOFORM 2).
CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.	RC	STRAIN=Wistar; TISSUE=Sertoli cells;
CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.	RX	MEDLINE=2050056; PubMed=10581401;
DR	Pfam: PF01150; GDAL_CD39_1.	RA	Vlajkovic S.M., Housley G.D., Greenwood D., Thorne P.R.; Evidence for alternative splicing of ecto-ATPase associated with termination of purinergic transmission. ";
DR	PROSITE: PS01238; GDAL_CD39_NTPASE; 1.	RT	Brain Res. Mol. Brain Res. 73:85-92(1999).
DR	KW Hydrolase; Transmembrane; Glycoprotein; Calcium; Magnesium; Alternative splicing.	RL	Brain Res. Mol. Brain Res. 73:85-92(1999).
FT	DOMAIN 1 4 CYTOPLASMIC (POTENTIAL).	CC	-!- FUNCTION: IN THE NERVOUS SYSTEM COULD HYDROLYZE ATP AND OTHER NUCLEOTIDES TO REGULATE PURINERGIC NEUROTRANSMISSION. HYDROLYZES ADP ONLY TO A MARGINAL EXTENT.
FT	TRANSMEM 5 25 POTENTIAL.	CC	-!- CATALYTIC ACTIVITY: ATP + H ₂ O = ADP + phosphate.
FT	DOMAIN 26 462 EXTRACELLULAR (POTENTIAL).	CC	-!- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.
FT	TRANSMEM 463 483 POTENTIAL.	CC	-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
FT	DOMAIN 484 495 CYTOPLASMIC (POTENTIAL).	CC	-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPlicing.
FT	CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).	CC	-!- SIMILARITY: BELONGS TO THE GDAL / CD39 NTPASE FAMILY.
FT	CARBOHYD 129 294 N-LINKED (GLCNAC. . .) (POTENTIAL).	CC	KIDNEY, SKELETAL MUSCLE, THYMUS, LUNG AND SPLEEN. WEAK EXPRESSION IN LIVER.
FT	CARBOHYD 294 319 N-LINKED (GLCNAC. . .) (POTENTIAL).	CC	-!- INDUCTION: BY FSH IN SEROTLI CELLS BUT NOT IN PERITUBULAR CELLS;
FT	CARBOHYD 319 378 N-LINKED (GLCNAC. . .) (POTENTIAL).	CC	BY CAMP IN BOTH TYPE OF CELLS.
FT	CARBOHYD 378 443 N-LINKED (GLCNAC. . .) (POTENTIAL).	CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.
FT	CARBOHYD 443 130 N-LINKED (GLCNAC. . .) (POTENTIAL).	CC	-!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, HEART, VAS DEFERENS, KIDNEY, SKELETAL MUSCLE, THYMUS, LUNG AND SPLEEN. WEAK EXPRESSION IN LIVER.
FT	CARBOHYD 130 133 MISSING (IN SHORT ISOFORM).	CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.
FT	CARBOHYD 133 400 T -> A (IN REF. 3).	CC	-!- SIMILARITY: BELONGS TO THE GDAL / CD39 NTPASE FAMILY.
FT	CONFLICT 400 414 S -> R (IN REF. 3).	CC	KIDNEY, SKELETAL MUSCLE, THYMUS, LUNG AND SPLEEN. WEAK EXPRESSION IN LIVER.
FT	CONFLICT 414 437 T -> A (IN REF. 3).	CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.
SO	SEQUENCE 495 AA: 5310 MW; CC0811CD90R4C8 CRC64;	CC	-!- INDUCTION: BY FSH IN SEROTLI CELLS BUT NOT IN PERITUBULAR CELLS;
SO	SEQUENCE 495 AA: 5310 MW; CC0811CD90R4C8 CRC64;	CC	the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content IS in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
DR	EMBL: AF275940; AAC87740_1.	CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.
DR	EMBL: AF275940; AAC87740_1.	CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.
DR	InterPro: IPR000407; GDAL_CD39_NTPase.	CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.
DR	Pfam: PF01150; GDAL_CD39_1.	CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.
DR	PROSITE: PS01238; GDAL_CD39_NTPASE; 1.	CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.
DR	KW Hydrolase; Transmembrane; Glycoprotein; Calcium; Magnesium; Alternative splicing.	CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.
FT	DOMAIN 1 4 CYTOPLASMIC (POTENTIAL).	CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.
FT	TRANSMEM 5 25 EXTRACELLULAR (POTENTIAL).	CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.
FT	DOMAIN 26 462 POTENTIAL.	CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.
FT	TRANSMEM 463 483 CYTOPLASMIC (POTENTIAL).	CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.
FT	DOMAIN 484 495 CYTOPLASMIC (POTENTIAL).	CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.
FT	CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).	CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.
FT	CARBOHYD 129 294 N-LINKED (GLCNAC. . .) (POTENTIAL).	CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.
FT	CARBOHYD 294 306 N-LINKED (GLCNAC. . .) (POTENTIAL).	CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.
FT	CARBOHYD 306 319 N-LINKED (GLCNAC. . .) (POTENTIAL).	CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.
FT	CARBOHYD 319 378 N-LINKED (GLCNAC. . .) (POTENTIAL).	CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.
FT	CARBOHYD 378 443 N-LINKED (GLCNAC. . .) (POTENTIAL).	CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.
FT	CARBOHYD 443 486 N-LINKED (GLCNAC. . .) (POTENTIAL).	CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.
FT	CARBOHYD 486 495 VRSKSPGAL->FLSPQLEQAPPTGNWESVPCLLVTKVFDKS (IN ISOFORM 2).	CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.
FT	CONFICT 20 20 T -> A (IN REF. 2).	CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.
FT	CONFICT 127 128 PP -> LL (IN REF. 2).	CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.
FT	CONFICT 339 339 A -> T (IN REF. 2).	CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.
FT	CONFICT 444 444 L -> F (IN REF. 2).	CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.
SO	SEQUENCE 495 AA: 54389 MW; 237B999F1BBB8ED0 CRC64;	CC	-!- PTM: HAS PROBABLY DISULFIDE BONDS.
Query Match	58.3%	RT	"An ecto-ATPase and an ecto-ATP diphosphohydrolase are expressed in Best Local Similarity 84.6%; Pred. No. 0.046;

Best Local Similarity 84.6%; Pred. No. 0.046;
 Query Match 58.3%; Score 56; DB 1; Length 495;
 Best Local Similarity 84.6%; Pred. No. 0.046;

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi.
 OC Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Rattus.
 OX NCBL_TAXID=10116;
 RN [1] SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=98031057; PubMed=936474;
 RA Kegel B., Braun N., Heine P., Maliszewski C.R., Zimmermann H.,

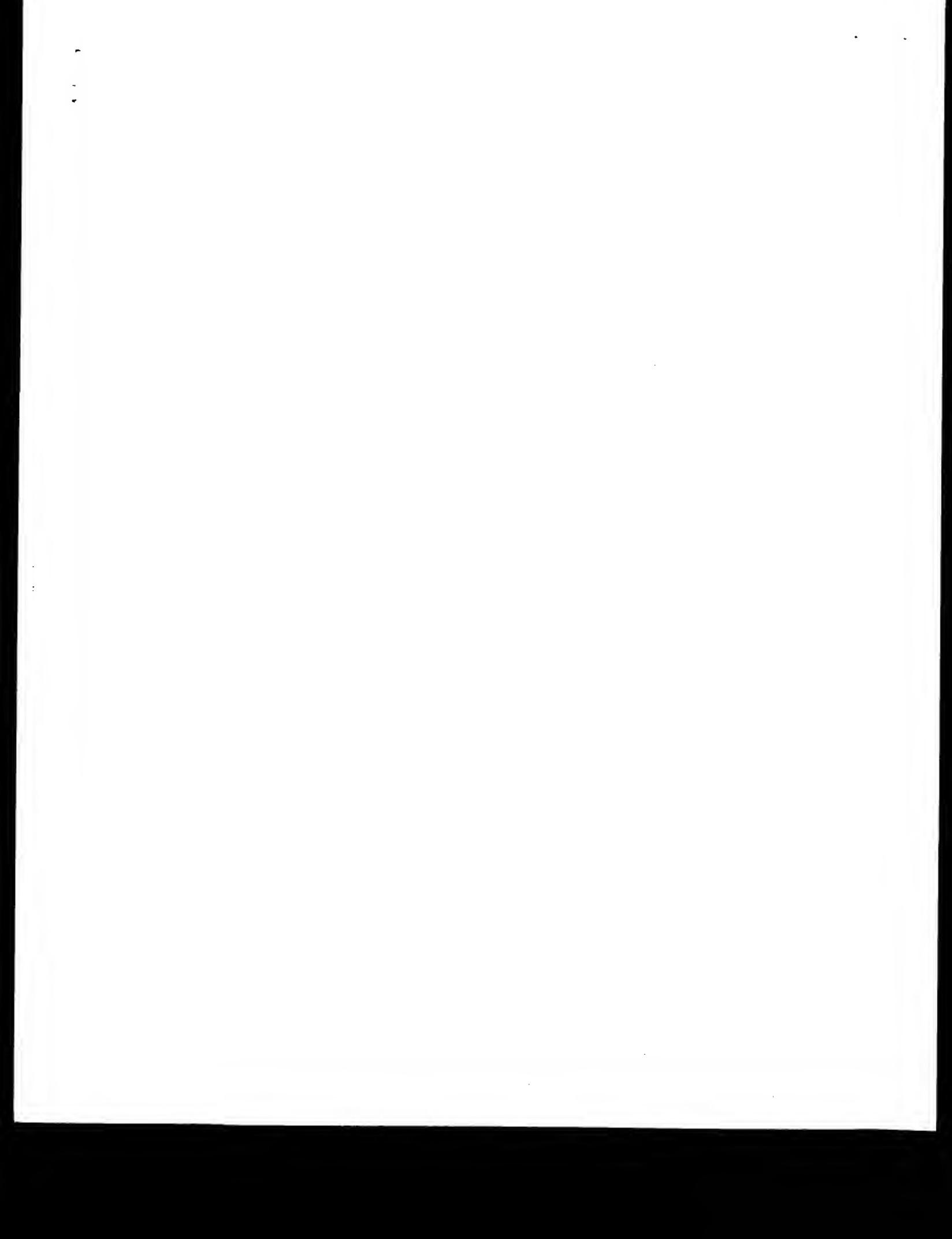
Wed Feb 12 11:36:09 2003

us-09-781-796b-7.rsp

Page 11

FT	DOMAIN	518	630	CYTOSOLIC (POTENTIAL).
SQ	SEQUENCE	630 AA:	71851 MW:	0288D2A78212544 CRC64;
Query Match		54.2%	Score 52;	DB 1; Length 630;
Best Local Similarity		69.2%	pred. No. 0; 3;	Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy	7 TYGALIDLEGASTQ	19		
Db	179 TFGFMDMGGASTQ	191	1:1 :1:11111	

Search completed: February 11, 2003, 18:38:00
Job time : 12 secs



GenCore version 5.1.3
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Om protein - protein search, using sw model
Run on: February 11, 2003, 18:33:31 ; Search time 92 seconds
(without alignments)
42.553 Million cell updates/sec

Title: US-09-781-796B-7
Perfect score: 96
Sequence: KSDPQETVGALDILGGASTQ 19

Scoring table: BILOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

- 1: SPTRMBL_21;*
- 2: SP_ARCHEA;*
- 3: SP_BACTERIA;*
- 4: SP_FUNGI;*
- 5: SP_HUMAN;*
- 6: SP_INVERTEBRATE;*
- 7: SP_MAMMAL;*
- 8: SP_ORGANELLE;*
- 9: SP_PHAGE;*
- 10: SP_PLANT;*
- 11: SP_RODENT;*
- 12: SP_VIRUS;*
- 13: SP_VERTREBRATE;*
- 14: SP_UNCLASSIFIED;*
- 15: SP_VIRUS;*
- 16: SP_BACTERIAP;*
- 17: SP_ARCHEAP;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	7.5	78.1	510 11	092106 Q921q6 mmu musculu
2	64	66.7	407 4	08WUB3 Q9wub3 homo sapien
3	64	66.7	428 4	096rx0 homo sapien
4	58	60.4	493 13	090X66 gallus gallus
5	58	60.4	681 10	08S613 oryza sativa
6	56	58.3	495 11	0921r1 mus musculus
7	54	56.2	300 11	090813 mus musculus
8	53	55.2	1052 10	049676 arabidopsis
9	51	53.1	3 091n35	09ut35 schizosaccharomyces pombe
10	49	51.0	483 10	093162 arabidopsis
11	48	50.0	447 10	09pu11 mus musculus
12	48	50.0	448 11	08R0ul mus musculus
13	48	50.0	462 10	09XFC9 dolichos biflorus
14	48	50.0	635 10	08s7f1 oryza sativa
15	47	49.0	467 10	08rvt6 plumbum sativum
16	47	49.0	606 11	09rt10 mus musculus

ALIGNMENTS

RESULT 1

ID	PRELIMINARY;	PRT;	510 AA.
092106			
AC	092106;		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	Similar to ectonucleoside triphosphate diphosphohydrolase 1.		
OS	Mus musculus (mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.		
RL	DR EMBL; BC011278; AAH11278; 1; -		
DR	DR Interpro; IPK00407; GDA1_CD39_NTPase.		
DR	PFAM; PF01150; GDA1_CD39; 1.		
DR	PROSITE; PS01238; GDA1_CD39_NTPase; UNKNOWN1.		
KW	Hydrolase.		
SQ	SEQUENCE 510 AA; 57176 MW; E7TB644AE143A0 CRC64;		

Query Match 78.1%; Score 75; DB:11; Length 510;
Best Local Similarity 83.3%; Pred. No. 0.00028;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 SDPQETVGALDILGGASTQ 19

RESULT 2

ID	PRELIMINARY;	PRT;	407 AA.
08WUB3			
AC	08WUB3;		
DT	01-MAR-2002 (TREMBLrel. 20, created)		
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		

DB	Similar to ectonucleoside triphosphate diphosphohydrolase 5.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID	9606;
RN	[1] SEQUENCE FROM N.A.
RP	TISSUE-COLON;
RC	Strausberg R.,
RA	Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RL	InterPro; IPR00407; GDA1_CD39_NTPase.
DR	Pfam; PF01150; GDA1_CD39_1.
DR	Hydrolease.
SEQUENCE	407 AA; 45336 MW; D92A5F7DC9EC9E5B CRC64;
Query Match	66.7%; Score 64; DB 4; Length 407;
Best Local Similarity	86.7%; Pred. No. 0.016;
Matches	13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY	5 QENYGALDGGASTQ 19
Db	192 QENVGTLDDGGASTQ 206
RESULT 3	SEQUENCE FROM N.A.
096RX0	PRELIMINARY; PRT; 428 AA.
ID	Q96RX0
AC	Q96RX0;
DT	01-DEC-2001 (TREMBrel. 19, Created)
DT	01-DEC-2001 (TREMBrel. 19, Last sequence update)
DT	01-MAR-2002 (TREMBrel. 20, Last annotation update)
DE	Proto-oncogene protein.
DE	Homo sapiens (Human).
OC	Mammalia; Eutheria; Primates; Cetartiodactyla; Hominoidea; Homo.
OC	Euksarota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID	9606;
RN	[1] SEQUENCE FROM N.A.
RP	MEDLINE=20173601; PubMed=10708485;
RA	Recio J.A., Zambrano N., Pena, Ld, Reig J.A., Rhoads A., Rouzaut A.,
RA	Notario V.,
RT	The human PCP8 proto-oncogene: cDNA identification, primary structure, chromosomal mapping, and expression in normal and tumor cells"; Mol. Carcinog. 27:229-236(2000).
RT	EMBL: AF136572; AAC82950.1; -.
DR	InterPro; IPR00407; GDA1_CD39_NTPase.
DR	Pfam; PF01150; GDA1_CD39_1.
SEQUENCE	428 AA; 47431 MW; F2C4F7DE65044F6 CRC64;
Query Match	66.7%; Score 64; DB 4; Length 428;
Best Local Similarity	86.7%; Pred. No. 0.018;
Matches	13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY	5 QETYGALDGGASTQ 19
Db	192 QETVGTLDGGASTQ 206
RESULT 5	SEQUENCE FROM N.A.
085613	PRELIMINARY; PRT; 681 AA.
ID	Q85613
AC	Q85613;
DT	01-JUN-2002 (TREMBrel. 21, Created)
DT	01-JUN-2002 (TREMBrel. 21, Last sequence update)
DT	01-JUN-2002 (TREMBrel. 21, Last annotation update)
DE	Putative nucleoside phosphatase.
DE	OSNBB0023M11.0.
OS	Oriza sativa (Rice).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidea; Oryzae; Oryza.
NCBI_TaxID	4530;
RN	[1] SEQUENCE FROM N.A.
RP	STRAIN=NIPPONBARE;
RC	McCormie W.R., de la Bastide M., Spiegel L., Preston R., Kirchoff K.,
RA	Kuit K., Nascentio L., Baker J., Santos L., Zutavien T., Miller B.,
RA	Cunnis D.M., Kattenberger F., Muller S., Bell M., Ballja V., Shah R.,
RA	King L., Yang C., Bilek S., O'Shaughnessy A., Palmer L., Dedilia N.;
RT	"Genomic sequence for Oryza sativa, Nipponbare strain, clone OSNBB0023M11, from chromosome 10, complete sequence";
RT	Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AC092749; AAM08556.1; -.
SEQUENCE	681 AA; 75002 MW; B1E874792202580BD CRC64;
Query Match	60.4%; Score 58; DB 10; Length 681;
Best Local Similarity	61.1%; Pred. No. 0.32;
Matches	11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
OY	2 SDDQTYGAHDGGASTQ 19
Db	260 SSSKMTYGSLLGGSSLQ 277
RESULT 6	SEQUENCE FROM N.A.
0921R1	PRELIMINARY; PRT; 495 AA.
ID	Q921R1
AC	Q921R1;
DT	01-DEC-2001 (TREMBrel. 19, Created)
DT	01-DEC-2001 (TREMBrel. 19, Last sequence update)
DT	01-JUN-2002 (TREMBrel. 21, Last annotation update)
DE	Ectonucleoside triphosphate diphosphohydrolase 2.
DE	ECto-ATP-diphosphohydrolase (EC 3.6.1.5).
OC	Calulus gallus (Chicken).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC	Gallus; Gallus; Gallus.
NCBI_TaxID	9031;
NCBI_TaxID	10090;

RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC011241; AAH11241.1; -.
 MGD; MGI:1096863; Entpd2.
 DR InterPro; IPR000407; GDAL_CD39_NTPase.
 DR Pfam; PF01150; GDAL_CD39; 1.
 DR PROSITE; PS01238; GDAL_CD39_NTPase; UNKNOWN_1.
 KW Hydrolase.
 SQ SEQUENCE 495 AA; 54319 MW; AT6468A0CBF86AAC CRC64;
 Query Match 58.3%; Score 56; DB 11; Length 495;
 Best Local Similarity 84.6%; Pred. No. 0.49;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 RT
 QY 7 TYGALDGGASTQ 19
 DB 196 TIGAMDGGASTQ 208
 RESULT 7
 ID 09D813 PRELIMINARY; PRT; 300 AA.
 AC 09D813; [3]
 DR 01-JUN-2001 (TREMBrel. 17, Created)
 DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DE 2010320H07Rik protein.
 GN OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Mus.
 OX NCBI_TaxID:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;
 RX MEDLINE=21085660; Published=1121-851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H., Ashburner M., Baralov S., Cassavant T.,
 RA Fleischmann W., Gaasterland T., Giessi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Niwaido I., Pesce G., Quackenbush J.,
 RA Schirali I.M., Staubli R., Suzuki R., Tomita M., Wagner L., Wasio T.,
 RA Sakai K., Okada T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carricchio P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarella J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sesaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Tovo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:687-690(2001);
 DR EMBL; AK008590; BAD2564.1; -.
 DR MGI; MGI:1919340; 2010320H07Rik.
 DR InterPro; IPR000407; GDAL_CD39_NTPase.
 DR Pfam; PF01150; GDAL_CD39; 1.
 SQ SEQUENCE 300 AA; 33646 MW; CCDE372AF12c6B16 CRC64;
 Query Match 56.2%; Score 54; DB 11; Length 300;
 Best Local Similarity 100.0%; Pred. No. 0.58;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RT
 QY 9 GALDGGASTQ 19
 DB 4 GALDGGASTQ 14
 RESULT 8

049676 ID 049676 PRELIMINARY; PRT; 1052 AA.
 AC 049676; [2]
 DR 01-JUN-1998 (TREMBrel. 06, Created)
 DT 01-JUN-1998 (TREMBrel. 06, Last sequence update)
 DT 01-OCT-2001 (TREMBrel. 18, Last annotation update)
 DE Hypothetical 116.4 kDa protein.
 GN T18B16.150 OR AtMG19180.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Baryonyx; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID:3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Bevan V., Recchmann S., Borkova D., Ansorge W., Meves H.W., Lemcke K.,
 RA Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AL01687; CAB16707.1; -.
 DR EMBL; AL16150; CAB78320.1; -.
 DR InterPro; IPR000620; DUF6.
 DR InterPro; IPR000407; GDAL_CD39_NTPase.
 DR Pfam; PF00892; DUF6; 1.
 DR Pfam; PF01150; GDAL_CD39; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 1052 AA; 116388 MW; 88C4AF1F16225987 CRC64;
 Query Match 55.2%; Score 53; DB 10; Length 1052;
 Best Local Similarity 76.9%; Pred. No. 3.9;
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 RT
 QY 7 TYGALDGGASTQ 19
 DB 685 TFGALDGGSSLQ 697
 RESULT 9
 ID 09UT35 PRELIMINARY; PRT; 556 AA.
 AC 09UT35; [2]
 DR 01-MAY-2000 (TREMBrel. 13, Created)
 DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBrel. 20, Last annotation update)
 DE Putative guanosine-diphosphatase (Guanosine diphosphatase).
 GN GNAUC824_08 GR_GDP1.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 OX NCBI_TaxID:4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=97H-; [2]
 RA Barrell B.G., Rojandream M.A., Quail M., Seagar K., Harris D.,
 RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Sanchez R., Franco A., Notario V., Gacto M., Cansado J.;
 RT "Characterization of a guanosine diphosphatase gene from
 Schizosaccharomyces pombe.",
 RT Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
 RL EMBL; AL12174; CAB7338.1; -.
 DR EMBL; AL46540; AL69974.1; -.
 DR InterPro; IPR000407; GDAL_CD39_NTPase.

DR Pfam: PF01150; GDAL_CD39; 1.
 DR PROSITE: PS01238; GDAL_CD39_NTpase; 1.
 SQ SEQUENCE 556 AA; 61588 MW; 1DB11ED6A6BBB5 CRC64;

Query Match 53.1%; Score 51; DB 3; Length 556;
 Best Local Similarity 62.5%; Pred No. 4;
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 TOETYGALDLGGASTQ 19
 Db 276 THSTVAVMDLGGASTQ 291

RESULT 10

09X162
 ID 09X162 PRELIMINARY; PRT; 483 AA.
 AC 09X162;
 DT 01-NOV-1999 (TREMBrel. 12, Created)
 DT 01-MAR-2002 (TREMBrel. 20, Last annotation update)
 DE F7A19_34 protein.
 GN F7A19_34.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TAXID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=CV. COLUMBIA;
 RA Federlspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
 RA Gonzalez A., Kremenevskaya T., Kim C., Ienz C., Li J., Liu S.,
 RA Lukacs S., Schwartz J., Shinn P., Toriumi M., Wysotskaya V.S.,
 RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
 RL Submitted (JUN 1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AC001576; AAD9311.1;
 DR InterPro: IPR001092; HHL_basic.
 DR Pfam: PF01150; GDAL_CD39; 1.
 DR PROSITE: PS01238; GDAL_CD39_NTpase; UNKNOWN_1.
 DR SEQUENCE PS001038; HELIX_LOOP_HELIX; UNKNOWN_1;
 SQ 483 AA; 53425 MW; 4E31D13830F1C8F9 CRC64;

Query Match 51.0%; Score 49; DB 10; Length 483;
 Best Local Similarity 55.6%; Pred No. 7.4;
 Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 SDTQETYGALDLGGASTQ 19
 Db 212 TDPLETTGIVELGGASQ 229

RESULT 11

09FULL
 ID 09FULL PRELIMINARY; PRT; 447 AA.
 AC 09FULL;
 DT 01-MAR-2001 (TREMBrel. 16, Created)
 DT 01-MAR-2001 (TREMBrel. 16, Last sequence update)
 DE Apyrase 2.
 GN APY2.

OS Pisum sativum (Garden pea).
 OC Fabikyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
 OX NCBI_TaxID=3808;
 RN [1]
 RP SEQUENCE FROM N.A.
 RN "Cloning of a Second Apyrase in Pisum sativum.";
 RT Submitted (SERB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF05783; AAG22044.1; -.
 DR MEDLINE=99254121; PubMed=10318974;
 RX Ezler M.E., Kalsi G., Ewing N.N., Roberts N.J., Day R.B.,
 RA Murphy J.B.;
 RT "A nod factor binding lectin with apyrase activity from legume
 roots";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:5856-5861(1999).
 DR EMBL; AF119807; AAD3185.1; -.
 DR InterPro: IPR00407; GDAL_CD39_NTpase.
 DR Pfam: PF01150; GDAL_CD39; 1.
 DR PROSITE: PS01238; GDAL_CD39_NTpase; 1.
 KW Hydrolase; Lectin.
 SQ SEQUENCE 462 AA; 51183 MW; 59865A9D4CC444B CRC64;

RESULT 12

09R01
 ID 09R01 PRELIMINARY; PRT; 448 AA.
 AC 09R01;
 DT 01-JUN-2002 (TREMBrel. 21, Created)
 DT 01-JUN-2002 (TREMBrel. 21, Last sequence update)
 DE Similar to lysosomal apyrase-like 1 (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TAXID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=KIDNEY;
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC026420; AAH26420.1; -.
 FT NON_TER
 SQ SEQUENCE 448 AA; 51285 MW; 0DA76F8BA734E3D6 CRC64;

Query Match 50.0%; Score 48; DB 11; Length 448;
 Best Local Similarity 60.0%; Pred No. 10;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 5 QETYGALDLGGASTQ 19
 Db 107 KRTAGVLDMGSGVSTQ 121

Query Match 50.0%; Score 48; DB 10; Length 462;
 Best Local Similarity 64.3%; Pred. No. 10;
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 3 DQQETYGALDGGSATQ 19
 | :| :| :| :| :| :| :|
 Db 210 DYSKTVGWDLGGGSVQ 226

Search completed: February 11, 2003, 18:39:40
 Job time : 94 secs

RESULT 14

Q857F1 PRELIMINARY; PRT; 635 AA.
 ID Q857F1:
 AC 0QS7FL:
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DE Putative apyrase.
 GN OSUNBB0048020.4.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina;
 OC Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 RN NMBI_TAXID=4530;
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV_NIPONBARE;
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
 RA Gansberger K., Bremer M., Burgess S., Hance M., Shvartsbeyn M.,
 RA Tsitrin T., Rigg F., Hsiao J., Lissmann V., Blunt S., Pai G.,
 RA Vanaken S.E., Utterback T.V., Kalb E., Quackenbush J.,
 RA Salzberg S.L., White O., Fraser C.M.;
 RT "Oryza sativa chromosome 3 BAC OSJNBB0048D20 genomic sequence.";
 RL Submitted (FEB 2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC084766; AAL82534.1; -.
 SQ SEQUENCE 635 AA; 6957 MM; 61E8F7B0D1EA4913 CRC64;

Query Match 50.0%; Score 48; DB 10; Length 635;
 Best Local Similarity 52.9%; Pred. No. 15;
 Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 OY 3 DQQETYGALDGGSATQ 19
 | :| :| :| :| :| :| :|
 Db 198 DPKHTGIGELGGASQ 214

RESULT 15

Q8RV76 PRELIMINARY; PRT; 467 AA.
 ID Q8RV76:
 AC 0QRVT6;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DE PAPY2.
 GN PAPY2.
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplanteae; Streptophytina; Embryophytina; Tracheophytina;
 OC Spermatophytina; Magnoliophytina; eudicotyledons; core eudicots; Rosidae;
 OC Fabales; Fabaceae; papilionoidae; Vicieae; Pisum.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV_MIDORISUI; TISSUE=DARK GREEN STEM;
 RA Kawahara T., Miura A., Kiba A., Toyota K., Ichinose Y., Shiraishi T.;
 RT "Characterization of pea Cell Wall-bound Apyrases.";
 DR Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 EMBL; AB071370; BAB85978.1; -.
 SQ SEQUENCE 467 AA; 50964 MW; 94167066C46E0D3C CRC64;
 Query Match 49.0%; Score 47; DB 10; Length 467;
 Best Local Similarity 52.9%; Pred. No. 16;
 Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

